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1 MRCLPVFVILLLLTASGPSV.....LQRHQDKSVCCGYKLCFPCG 62 US-10-072-602B-352 331 score: Sequence: Perfect

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1586107 Total number of hits satisfying chosen parameters:

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Listing first 45 summaries

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### ALIGNMENTS

ABG99600 standard; protein; 62 AA.

ABG99600;

(first entry) 17-JAN-2003

Conus sp conotoxin-associated protein SEQ ID 352.

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.

Conus aulicus.

WO200264740-A2.

22-AUG-2002.

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P

(COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.

Garrett JE, Cruz LJ; es RM, Schoenfeld RM; Watkins M, Garret' letty R, Jones RM, Olivera BM, Mcintosh JM, Watkins Grilley M, Walker CS, Shetty R,

2002-706921/76.

WPI; 2002-706921/ N-PSDB; ABX04937.

New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

Claim 1; Page 239; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be pain in an individual who is either exhibiting pain or is about to be poin in an individual who is either exhibiting pain or is about to be poin in an admin-gaussing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for 

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characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
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ligand-gated ion channel modulator; pain-relief.
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stty R, Jones RM, Schoenfeld RM;
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                                                                                                                                          Score 331; DB 5;
Pred. No. 4.8e-35;
0; Mismatches 0;
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100.0%;
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UNIV UTAH RES FOUND
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                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP
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etty R, Jones RM, Schoenfeld
                                                                                     Indels
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                                                      Score 298; DB 5;
Pred. No. 8.9e-31;
4; Mismatches 3;
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in the disclosure of the invention
                                                                                                                                                                                                                                                                                    ABG99589 standard; protein; 62 AA.
                                                         90.0%;
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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated in channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders. The radiolabeled conotoxin peptide is also useful for channel disorders, ligand-gated conotoxin peptide is also useful for channel disorders in the disorders mail molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
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                                                                              1 MRCLPVFVILLLIASGPSVDARLKIKDDVPLSSFRDNAKSTLQRLQDKRLCCGFWMCIP
                                                                                                                                                                                                                                                                                                                                                                               snail; analgesic; voltage-gated ion channel modulator;
                                                               1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP
                                  Gaps
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Length 62;
                                4; Indels
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Jones RM, Schoenfeld
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Score 286; DB 5;
Pred. No. 3.2e-29;
3; Mismatches 4;
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86.4%;
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(UTAH ) UNIV UTAH RES FOUND.
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                              54; Conservative
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Matches 54; Conserv
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MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
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ligand-gated ion channel modulator; pain-relief.
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Malker CS, Shetty R, Jones RM, Schoenfeld
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                                                                                                                                                                                                                                                                            Conus sp conotoxin-associated protein SEQ ID 358.
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Gaps

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84.9%; Score 281; DB 5; Length 62; 82.3%; Pred. No. 1.4e-28; ive 6; Mismatches 5; Indels

Best Local Similarity 82.3 Matches 51; Conservative

Query Match

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Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
                                                                                                              Conus sp conotoxin-associated protein SEQ ID 361.
                                     ABG99606 standard; protein; 62 AA.
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                                                                                                                                                                                                                                                                                                      (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                                             Conus ammiralis.
                                                                                                                                                                                                       WO200264740-A2.
                                                                                      17-JAN-2003
                                                                                                                                                                                                                                                                                                                                              Olivera BM,
                                                                                                                                                                                                                             22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                          Grilley M,
                                                              ABG99606;
                         ABG99606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The concotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRCLPVFVILLLLTASGPSVDAR--LKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG93360-ABG99863 represent the conotoxin protein and peptides described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion
                                                                                                                                                                                        Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
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etty R, Jones RM, Schoenfeld RM;
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Pred. No. 2.2e-27;
                                                                                                                                                                 Conus sp conotoxin-associated protein SEQ ID 342
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                                                                                                                                                                                                                                                                                                                                                                                                            Shetty R,
                                                                                       ABG99593 standard; protein; 64 AA.
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                                                                                                                                                                                                                                                                                                         11-FEB-2002; 2002WO-US003887.
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Best Local Similarity
                                                                                                                                                                                                                                Conus episcopatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABX04934.
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CG 62
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                                                                                                                                         17-JAN-2003
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                         61
                                                                                                                ABG99593
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Matches
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1, Watkins M, Garrett JE, Cruz Shetty R, Jones RM, Schoenfeld

Mcintosh JM,

Walker CS,

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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders. In adiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.
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Pred. No. 1.2e-26;
4; Mismatches 7; Indels
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59 FPCG 62

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61 VPCG

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genus Conus which have an algand-gated ion channel modulator or a ligand-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders. Itseating or preventing disorders associated with voltage-gated ion disorders. The radiolabeled conotoxin peptide is also useful for characterising an new site on these receptors or channels, and for soreening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99833 represent the conotoxin protein and peptides described in the disclosure of the invention
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Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld
                  Conus sp conotoxin-associated protein SEQ ID 333.
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                                                                                     ligand-gated ion channel modulator; pain-relief
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N-PSDB; ABX04931.
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                                                                Conotoxin;
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ID ABG9
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ligand-gated ion channel modulator; pain-relief.
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es RM, Schoenfeld RM;
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                                                                                                     conotoxin-associated protein SEQ ID 162
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etty R, Jones RM,
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Olivera Grilley

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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conocoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP
                                                                                                                                                                                                                                Watkins M, Garrett JE, Cruz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 254.5; DB 5;
Pred. No. 3.7e-25;
1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus sp conotoxin-associated protein SEQ ID 370.
                                                                                                                                                                                                                                                 Shetty R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 218; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG99612 standard; protein; 61 AA.
                                                                                     11-FEB-2002; 2002WO-US003887.
                                                                                                                            09-FEB-2001; 2001US-0267408P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.2%;
Matches 52; Conservative 1
                                                                                                                                                                  (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                Ę,
                                                                                                                                                                                                                                                 Walker CS,
                                                                                                                                                                                                                                Mcintosh
                                                                                                                                                                                                                                                                                          2002-706921/76.
                                                                                                                                                                                                                                                                                          WPI; 2002-706921/
N-PSDB; ABX04918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61 AA;
      WO200264740-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus omaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2003
                                            22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG99612;
                                                                                                                                                                                                                                Olivera |
Grilley |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoantme transporters.
                                                                                                                                                                                                                                                                                                                                                                                                                        New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRCLPVFVILLLITASAPSVDAKVHLKTKGDGPLSSFRDNAKSTLQRLQDKSTCCGFKMC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRCLPVFVILLLITASGPSVDAR--LKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                           Watkins M, Garrett JE, Cruz LJ;
etty R, Jones RM, Schoenfeld RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus sp conotoxin-associated protein SEQ ID 294.
ligand-gated ion channel modulator; pain-relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 264; DB 5;
Pred. No. 2.3e-26;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                  Shetty R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 242; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG99561 standard; protein; 61 AA
                                                                                                                                                                11-FEB-2002; 2002WO-US003887.
                                                                                                                                                                                                      09-FEB-2001; 2001US-0267408P.
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82.5%;
                                                                                                                                                                                                                                                 -) COGNETIX INC.
) UNIV UTAH RES FOUND.
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                                                                                                                                                                                                                                                                                                           Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                Walker CS,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-706921/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABX04941.
                                        Conus pennaceus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 FPC 61
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                                                                                 WO200264740-A2
                                                                                                                                                                                                                                                                                                             BM,
                                                                                                                       22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
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9

Gaps

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Indels

Query Match Best Local S

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WO200264740-A2

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.

Conus omaria

ABG99561;

RESULT 11 ABG99561

g

22-AUG-2002.

DB 5; Length 61;

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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful contracting or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders. The radiolabeled conotoxin peptide is also useful for characterising an new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the
                                                                                                                                                                                                        New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus sp conotoxin-associated protein SEQ ID 306.
                                                                                                                                                                                                                                                                                     Claim 1; Page 244; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG99569 standard; protein; 60 AA.
 11-FEB-2002; 2002WO-US003887
                                 09-FEB-2001; 2001US-0267408P
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                                                             (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                ĞM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                             Mcintosh J
Walker CS,
                                                                                                                                                           2002-706921/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 51, Conserv
                                                                                                                                                                         N-PSDB; ABX04943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus aulicus
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                                                                                                               ΒW,
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                                                                                                               Olivera I
Grilley N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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7;

Pred. No. 5e-2 2; Mismatches

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New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated don channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channel disorders, ligand-gated ion channel disorders or receptor adiocates. The radiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99863 represent the conotoxin protein and peptides described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                          Watkins M, Garrett JE, Cruz LJ;
letty R, Jones RM, Schoenfeld RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cruz LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 220; DB 5;
Pred. No. 1.1e-20;
1; Mismatches 12,
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                                                                                                                          Shetty R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG99400 standard; protein; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 222; 305pp; English.
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(COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
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                                                                                             Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                             Walker CS,
                                                                                                                                                                                    WPI; 2002-706921/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                     N-PSDB; ABX04922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60 AA;
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                                                                                             BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2003
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                                                                                          Olivera
                                                                                                                          Grilley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG99400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                           1, Watkins M, Garrett JE, Cruz LJ;
Shetty R, Jones RM, Schoenfeld RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.6%; Score 253.5; DB 5; Length 61; 83.6%; Pred. No. 5e-25;
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New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.
                                                                                                                                                                                                               genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator. The conoccarinel modulator or a ligand-gated ion channel modulator. The conoccarin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-canaing event. The conocoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the
                                                                                                                                                                                                                                                                                                                                                                                 above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
ligand-gated ion channel modulator; pain-relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel conotoxin peptides from the cone snail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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netty R, Jones RM, Schoenfeld RM;
Shetty R, Jones RM, Schoenfeld RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%; Score 216; DB 5; Length 61 68.9%; Pred. No. 3.6e-20; ive 3; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus sp conotoxin-associated protein SEQ ID 349.
                                                                                                                                                                                                                                                                                                                                                                                                                   in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shetty R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG99598 standard; protein; 61 AA.
                                                                                                                                                                  Claim 1; Page 130; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2002; 2002WO-US003887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-2001; 2001US-0267408P
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Walker CS, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Conservative
 Walker CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
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N-PSDB; ABX04936.
                                  WPI; 2002-706921/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                   N-PSDE; ABX04847
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ပ
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 Grilley M,
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genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders. Ingand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterising an new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ARG993860-ABG99883 represent the conotoxin protein and peptides described in the disclosure of the invention
                                           alleviating pain in an individual suffering from pain or who is about to
be subjected to a pain-causing event, or for treating voltage-gated ion
                                                                                                                                                                                                                   This invention describes novel conotoxin peptides from the cone snail.
                       snail conotoxin peptides, useful as a pain reliever for
                                                                                                                                                               Claim 1; Page 237; 305pp; English.
                                                                                                           channel disorders
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Sequence 61 AA;

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                                                                                                1 MRCLPVLIILLLITASARGVDVLPKTEDDVPLSSVXDNTKSILRGLDKRACCGYKLCSP
                                                                            1 MRCLPVFVILLLLIASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP
                                        Gaps
                                          ô
65.3%; Score 216; DB 5; Length 61; 68.9%; Pred. No. 3.6e-20; ive 3; Mismatches 16; Indels
    Query Match
Best Local Similarity 68.9
Matches 42; Conservative
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oleted: August 10, 2004, 16:02:37 81.4324 secs completed: time Search Job tim us-10-072-602b-352.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 10, 2004, 16:00:55 ; Search time 24.2973 Seconds (without alignments) 131.735 Million cell updates/sec Run on:

331 1 MRCLPVFVILLLLTASGPSV......LQRHQDKSVCGGYXLCFPCG 62 US-10-072-602B-352 Perfect score:

Sequence:

**BLOSUM62** Scoring table: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters:

Gapop 10.0 , Gapext 0.5 Searched:

389414

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

1: /cgr2\_6/prodata/2/iaa/5A COWB.pep:\*
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/prodata/2/iaa/6A COMB.pep:\*
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/prodata/2/iaa/PCTUS COMB.pep:\*
6: /cgn2\_6/prodata/2/iaa/PCTUS COMB.pep:\* Issued Patents AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	Sequence 37, Appl	39,	, c	Sequence 49. Appl	equence 43,		25.	equence 41,	equence 31,	33.	45	equence 23,	29.	equence 47.	27		111,	111,	111,	11172	11138,	11,	ω,	8	8	8	
SUMMARIES	ID	-09-497-491-3	US-09-497-491-39	US-09-497-491-35	09-497-491-4	-09-497-491-4	19-497-491-2	US-09-497-491-25	-09-497-491-4	9-497-4	-497-491-3	US-09-497-491-45	91-2	9-497-491-2	US-09-497-491-47	9-497-491-2	US-08-456-265A-111	US-08-971-217-111	US-09-350-600-111	9	9-489-	US-09-489-039A-11138	US-08-290-731C-11	-60-	US-09-245-281-8	US-09-207-359B-8	US-09-340-620A-8	US-09-865-364-8
	DB	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	Н	7	m	4	4	4	7	4	4	4	4	4
	Query Match Length	59	9	7.0	62	63	62	62	64	67	67	62	61	61	63	62	111	111	111	111	216	312	423	953	953	953	953	953
*	Query	62.2	60.1	60.1	54.5	•	51.2		20.6	50.5	50.2	49.5	45.8		44.7	39.1	17.8	17.8	17.8	17.8	17.2					ė.		16.8
	Score	206	199	199	180.5	179	169.5		167.5	167	166	164	151.5	151.5	148	129.5	59	29	29	59	57	55.5	55.5	55.5	55.5	55.5	55.5	55.5
	Result No.	. ~	7	m	4	S	9	7	æ	9	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25	26	27

Sequence 4, Appli	Sequence 20867, A	Sequence 3, Appli				7	'n	N	797			2	'n	110	Sequence 110. App	110	110,
US-08-290-731C-4	US-09-252-991A-20867	US-09-029-603-3	US-09-543-681A-6220	US-08-857-076-105	US-08-543-881-2	US-08-291-299-2	PCT-US94-00119-2	PCT-US95-10579-2	US-09-543-681A-7970	US-09-252-991A-24690	US-08-318-831-8	US-09-354-147C-2	US-09-354-147C-3	US-08-456-265A-110	US-08-971-217-110	US-09-350-600-110	US-09-906-234-110
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16	16	16.5	16	16	16	16	16	16	15	15	15	15.9	15	15	15	15	15
55.5	55.5	54.5	53.5	53.5	53	53	53	53	52.5	52.5	52.5	52.5	52.5	25	52	25	25
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

```
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hopper, David
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Robert M.
TITLE OF INVENTION: Tau-Conopetides
CURRENT APPLICATION NUMBER: US/09/497,491
CURRENT APPLICATION NUMBER: US 60/118,642
EARLIER APPLICATION NUMBER: US 60/118,642
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 37
LENGTH: S9
MANDER PATENTING DATE: 1999-02-04
SEQ ID NO 37
LENGTH: S9
MANDER PATENTING DATE: 1000-02-04
SEQ ID NO 37
LENGTH: S9
                         Sequence 37, Application US/09497491
Patent No. 6630573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus marmoreus
                                                                            GENERAL INFORMATION:
US-09-497-491-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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Gaps ; 0 Query Match 62.2%; Score 206; DB 4; Length 59; Best Local Similarity 70.7%; Pred. No. 4.2e-20; Matches 41; Conservative 5; Mismatches 12; Indels

;

1 MRCLPVFVILLLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58 Sequence 39, Application US/09497491
Patent No. 6630573
GENERAL INFORMATION:
APPLICANT: Walker, Craig
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hooper, David
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Steele, Doug
APPLICANT: Steele, Doug
APPLICANT: Steele, Tan-Conoperties
FILE REPERENCE: Tan-Conoperties
FILE REPERENCE: Tan-Conopepties
CURRENT APPLICATION NUMBER: US/09/497,491 US-09-497-491-39 ò 셤

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                                                                                                                                                                                                                                                         Length 60;
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                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                       60.1%; Score 199; DB 4; Lilarity 75.5%; Pred. No. 3.6e-19; Conservative 4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ratem. Nu. 00.20.5/3.

GRERAL INCORMATION:
APPLICANT: Walker, Craig
APPLICANT: Shetry, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hooper, David
APPLICANT: Hooper, David
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497, 491
CURRENT FILING DATE: 2000-02-04
EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ. DI NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Tau-Conotoxin Peptides
FILE REFERENCE: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497,491
CURRENT FILING DATE: 2000-02-04
EARLIER APPLICATION NUMBER: US 60/118,642
EARLIER FILING DATE: 1999-02-04
CURRENT FILING DATE: 2000-02-04
EARLIER APPLICATION NUMBER: US 60/118,642
EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 60
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. Sequence 49, Application US/09497491
. Patent No. 6630573
. GENERAL INFORMATION:
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; Sequence 35, Application US/09497491
; Patent No. 6630573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hooper, David
APPLICANT: Jacobsen, Richard
APPLICANT: Steele, Doug
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Conus marmoreus US-09-497-491-35
                                                                                                                                                                TYPE: PRT ORGANISM: Conus marmoreus
                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 40; Conserv
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US-09-497-491-39
                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                         1 MRCLPVFVILLLIASAPSVDAQPKTKDDVPLAPLHDNIRSTLQTLR-KKVCC
                                                                                                                                                                                                                                                                                           1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                                                                                                                                                                                       Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.1%; Score 179; DB 4; Length 63; 61.0%; Pred. No. 1.7e-16; ive 4; Mismatches 19; Indels
                                                                                                                                                                                          Score 180.5; DB 4
Pred. No. 1.1e-16;
4; Mismatches 10
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Sequence 21, Application US/09497491
Patent No. 6630873
GENERAL INFORMATION:
APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Hooper, David
APPLICANT: Hooper, David
APPLICANT: Hooper, David
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Doug
APPLICANT: Jacobsen, Doug
APPLICANT: Jacobsen
TITLE REFERENCE: Tau-Comopeptides
CURRENT PLING DATE: 2000-02-04
EARLIER PELLING DATE: 1999-02-04
NUMBER: OF SEQ ID NOS: 49
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, David
APPLICANT: Jacobsen, Richard
APPLICANT: Seele, Doug
APPLICANT: Seele, Doug
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Tau-Conopeptides
FILE REFERENCE: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497,491
CURRENT FILING DATE: 2000-02-04
EARLIER APPLICATION NUMBER: US 60/118,642
EARLIER PLING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, Application US/09497491
Patent No. 6630573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Conus caracteristicus
                                                                                                                                                                                            Query Match
Best Local Similarity 71.7%;
Matches 38; Conservative
                                                                                                ; TYPE: PRT; ORGANISM: Conus gloriamaris
US-09-497-491-49
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Conservative
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-497-491-43
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                                                                         LENGTH: 62
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Gaps

Indels

DB 4; Length 64;

50.6%; Score 167.5; DB 4 61.4%; Pred. No. 5.7e-15; iive 6; Mismatches 15

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Conservative
                                                         Best Local Similarity
Matches 35; Conserv
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US-09-497-491-33
       US-09-497-491-41
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LENGTH: 67
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                             1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                             Score 169.5; DB 4; Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 169; DB 4; Length 62;
Pred. No. 3.5e-15;
5; Mismatches 18; Indels
                                                                                                                               Indels
                                                                                                          Pred. No. 3e-15;
5; Mismatches 15;
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shetty, Reshma
APPLICANT: Othera, Baldomero M.
APPLICANT: Jacobsen, Baldomero M.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
ITLE OF INVENTION: Tau-Conopeptides
FILE REFRENCE: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497,491
CURRENT FILING DATE: 2000-02-04
EARLIER APPLICATION NUMBER: US 60/118,642
EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Tau-Conotoxin Peptides
FILE REFERENCE: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497,491
CURRENT FILING DATE: 2000-02-04
BARLIER FILING DATE: 1999-02-04
BARLIER FILING DATE: 1999-02-04
SOFTWARE: PACENTIN ONS: 49
                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09497491
Patent No. 6630573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/09497491
Patent No. 6630573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hooper, David
APPLICANT: Steele, Doug
APPLICANT: Steele, Doug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Conus característicus
                                                                                       ch 51.2%;
1 Similarity 63.8%;
37; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.1%;
60.3%;
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Best Local Similarity 60.33
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus quercinus US-09-497-491-25
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Conus textile
US-09-497-491-21
                                                                                                                                                                                                                                                                               US-09-497-491-25
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LENGTH: 62
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                                                                                           Query Match
Best Local
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                                                                                                                            Matches
                                                                                                                                                                                                                                                          RESULT 7
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1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKL 57
                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.5%; Score 167; DB 4; Length 67; 62.3%; Pred. No. 7.1e-15; tive 4; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 67;
                                                                                                                                                                                                                  APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Jacobsen, Richard
APPLICANT: Steel-, Doug
APPLICANT: Steel-, Doug
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497, 491
CURRENT APPLICATION NUMBER: US 60/118, 642
EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hooper, David
APPLICANT: Steele, David
APPLICANT: Steele, Doug
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Tau-Conocoxin Peptides
FILE REFERENCE: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497,491
CURRENT FILING DATE: 2000-02-04
BARLIER APPLICATION NUMBER: US 60/118,642
EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                           Sequence 31, Application US/09497491
Patent No. 6630573
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Patent No. 6630573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Conus textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Conus textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 33; Conserv
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1 MCCLPVFVILLLITSAPSVDALPKTRDDVPLASFHGGYNARRILQRRQGWCCKENIACC 60
                                        1 MCCLPVFVILLLITSAPSVDALPKTRDDVPLASFHGGYNARRILQRRQGWCCKENIACC 60
MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRD--NAKSTLQRHQ-----DKSVCC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRCLPVFVILLLITASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 151.5; DB 4;
Pred. No. 7e-13;
4; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 148; DB 4;
Pred. No. 2.1e-12;
7; Mismatches 15
                                                                                                                                                                                                                                                                                                                   GENERAL INVOCATION.

JUNEAR INVOCATION.

APPLICANT: Shetty, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Tau-Conopoptides
FILE REFERENCE: Tau-Conopoptides
CURRENT APPLICATION NUMBER: US/09/497, 491
CURRENT FILING DATE: 2000-02-04
BARLIER APPLICATION NUMBER: US 60/118, 642
BARLIER FILING DATE: 1999-02-04
SOFTWARE: PATENTIN ONS: 49
SOFTWARE: PATENTIN ONS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFOGRATION.

JAPPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Baldomero M.
APPLICANT: Juvera, Baldomero M.
APPLICANT: Jacobsen, Richard
APPLICANT: Steele, Doug
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Tau-Conopeptides
CURRENT APPLICATION NUMBER: US/09/497, 491
CURRENT FILING DATE: 2000-02-04
BARLIER APPLICATION NUMBER: US 60/118, 642
BARLIER PILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                             ; Sequence 29, Application US/09497491; Patent No. 6630573; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application US/09497491; Patent No. 6630573; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.7%;
58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cn 45.8%;
l Similarity 58.3%;
35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Conus geographus US-09-497-491-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
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Best Local Similarity
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Best Local Similarity
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                                                                                                      53
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                                                                                                                                                                1 MRCFPVFIILLILIASAPCFDARTKTDDDVPLSSLRDNLKRTIRTRLNIRGCC
                                                                                                      1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 62;
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Pred. No. 1.6e-14;
5; Mismatches 19; Indels
                                     Indels
   62.3%; Pred. No. 9.6e-15;
ive 4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                             GACHLAN, W., W.). WOJUSY, S., GENERAL INCRMATION:
APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hooper, David
APPLICANT: Hooper, David
APPLICANT: Jacobsen, Richard
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hooper, David
APPLICANT: Steele, Doug
APPLICANT: Steele, Doug
APPLICANT: Steele, Doug
APPLICANT: Steele, Doug
FILE REFERENCE: Tau-Conotoxin Peptides
FILE REFERENCE: Tau-Conotoxin Peptides
CURRENT APPLICATION NUMBER: US 69/497,491
CURRENT FILING DATE: 2000-02-04
RARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 61
                                                                                                                                                                                                                                                                                                                         Sequence 45, Application US/09497491
Patent No. 6630573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09497491
Patent No. 6630573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.6%;
Matches 34; Conservative
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Best Local Similarity 58.3%;
Matches 35; Conservative
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   Similarity 62.3 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Conus quercinus
US-09-497-491-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     US-09-497-491-45
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   Best Local
Matches
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Gaps

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RESULT 15
US-09-497-491-27
i Sequence 27, Application US/09497491
i Sequence 27, Application US/09497491
i Sequence 27, Application US/09497491
i Patent No. 650573
i GENERAL INFORMATION:
APPLICANT: Walker, Craig
APPLICANT: Steety, Reshma
APPLICANT: Olivera, Baldomero M.
APPLICANT: Steety, Doug
APPLICANT: Steele, Doug
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Search completed: August 10, 2004, 16:05:36 Job time: 25.2973 secs

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291, App 345, App 285, App 287, App 303, App 300, App 287, App 524, App 529, App 534, App 533, App 533, App 521, App 521, App 521, App 521, App 522, App 522, App 522, App 522, App 522, App 522, App

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ALIGNMENTS

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2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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ougnetix, Inc.
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McIntosh, J. Michael
Watkins, Maren
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Schoenfeld, Robert M.
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SOFTWARE: PatentIn version 3.0
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                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 336 LENGTH: 62
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Best Local Similarity 88.5%;
Matches 54; Conservative
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, ORGANISM: Conus pennaceus
US-10-072-602B-336
NUMBER OF SEQ ID NOS: 638
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Marchis, Baldomero M.
APPLICANT: Matkins, Maren
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Grilley, Michelle
APPLICANT: Schemfeld, Robert M.
APPLICANT: Cones, Robert M.
APPLICANT: Onnes, Robert M.
TITLE OF INVENTION: Cone Smail Peptides
FILE REFERENCE: 2314-249
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: Martines, Maren APPLICANT: Watkins, Maren APPLICANT: Grarrett, James E. APPLICANT: Grailey, Michaele APPLIC
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CURRENT FILING DATE: 2002-02-11
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CURRENT APPLICATION NUMBER: US/10/072,602B
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PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
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PRIOR PAPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SECTWARR: Patentin version 3.0
LENGTH: 62
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                                                                                                                                                                                                                                                                  Sequence 339, Application US/10072602B
Publication No. US20030109670A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Conus pennaceus
US-10-072-6028-339
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61 CG 62
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US-10-072-602B-336
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Score 286; DB 14; Length 62;
Pred. No. 1.1e-27;
3; Mismatches 4; Indels
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Pred. No. 4.6e-27;
6; Mismatches 5;
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APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
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CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
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APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
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; Publication No. US20030109670Al
; GENERAL INFORMATION:
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Cognetix,
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61 CG 62
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APPLICANT:
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Best Local Similarity 84.4%; Pred. No. 2e-26;
Matches 54; Conservative 3; Mismatches
         APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Graig C. Towards J.
APPLICANT: Graig Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE REFERENCE: 2314-249
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 358
LENGTH: 62
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APPLICANT: Schoenfeld, Robert M.
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
TITLE OF INVENTION CONE Snail Peptides
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PATENTIN VERSION 3.0
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o. US20030109670A1
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Cruz, Lourdes J.
McIntosh, J, Michael
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Best Local Similarity
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CG 62
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APPLICANT:
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1 MRCLPVFVILLLLTASGPSVDAKVHLKTKGDGPLSSFRDNAKSTLQRLQDKSTCCGYRMC 60
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Pred. No. 3.3e-25;
4; Mismatches 7; Indels
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CURRENT FILING DATE: 2002-02-11
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APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
PRIOR APPLICATION NUMBER: US/6267,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,409
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 361
LENTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
                                                                                                                                                                                             Sequence 361, Application US/10072602B Publication No. US2003109670A1 GENERAL INFORMATION:
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Publication No. US20030109670A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
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McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
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Grilley, Michelle
Schoenfeld, Robert M.
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Grilley, Michelle
Schoenfeld, Robert M.
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Query Match
Best Local Similarity
Matches 52; Conserv
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APPLICANT:
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                                                                                                                                                               Score 264; DB 14; Length 64;
Pred. No. 6e-25;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence ..., US20030LU90.v...
FUBLication No. US20030LU90.v...
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: APPLICANT: Mointosh, J. Michael
NDT.ICANT: Watkins, Maren
TOT.ICANT: Watkins, Maren
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Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
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APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFRENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT APPLICATION NUMBER: US 60/267,408
PRIOR PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SERVINGE: 64
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Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert M.
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 162
LENGTH: 64
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Best Local Similarity 82.5%;
Matches 52; Conservative
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US-10-072-602B-333
                                                                                              TYPE: FRT
ORGANISM: Conus pennaceus
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US-10-072-602B-333
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APPLICANT:
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Pred. No. 6e-25;
3; Mismatches 6; Indels
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Pred. No. 8.4e-24;
1; Mismatches 7;
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                                                                                                                                             APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR PILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REPERENCE: 2314-249
CURRENT APPLICATION MVBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 294, Application US/10072602B Publication No. US20030109670A1 GENERAL INFORMATION:
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Olivera, Baldomero M.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert M.
Olivera, Baldomero M.
McIntosh, J, Michael
Watkins, Maren
Garrett, James E.
                                                                                    Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert
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Best Local Similarity 85.2%;
Matches 52; Conservative
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82.5%;
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Query Match
Best Local Similarity
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1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
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                                                                                                                                                                         Sequence 370, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Markins, Maren
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Gruz, Lourdes J.
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Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE ON TITLE OF STATE THE SPERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
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TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILLING DATE: 2002-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
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Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Cruz, Lourdes J.
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Schoenfeld, Robert M.
Walker, Craig
Shetty, Reshma
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SOFTWARE: PatentIn version 3.0
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51; Conservative
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US-10-072-602B-370
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LENGTH: 61
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APPLICANT:
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APPLICANT:
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Best Local S
Matches 51
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APPLICANT:
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APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIncel
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
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Pred. No. 4.7e-19;
3; Mismatches 16;
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APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TILE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION WUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
NUMBER OF SEQ ID NOS: 638
SEQ ID NO 62
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SCFTWARE: Patentin version 3.0
SEQ ID NO 306
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-072-602B-349
Sequence 349, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 62, Application US/10072602B
Publication No. US20030109670A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert M.
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68.9%;
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Best Local Similarity 75.8°
Matches 47; Conservative
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ORGANISM: Conus bandanus
                                                                                                                                                           ORGANISM: Conus aulicus
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Query Match 65.3%; Score 216; DB 14; Length 61; Best Local Similarity 68.9%; Pred. No. 4.7e-19; Matches 42; Conservative 3; Mismatches 16; Indels
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J, Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James B.
APPLICANT: Garriley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
FILE REFERENCE: 2314-249
CURRENT FILING DATE: 2002-02-11
PRICR APPLICATION NUMBER: US 60/267,408
CURRENT FILING DATE: 2001-02-09
CURRENT FILING DATE: 2001-02-09
NUMBER OF SCO ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 349
LEMCTH: 61
TYPE: PRT
CREATION SANISM: Conus bandanus
US-10-072-602B-349
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Search completed: August 10, 2004, 16:13:54 Job time: 68.8649 secs

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0; Gaps

1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60 

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

August 10, 2004, 16:00:00; Search time 19.2703 Seconds (without alignments) 309.486 Million cell updates/sec Run on:

US-10-072-602B-352 Title: Perfect score:

331 1 MRCLPVFVILLLLTASGPSV.....LQRHQDKSVCCGYKLCFPCG 62 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283366 seqs, 96191526 residues

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:\* Database

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ф			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	188	- 9		1	F59147	Conotoxin DR 1 ave
N	180.5	4.	62	7	D59147	Oxin Gm5 2
ന		51.2	62	ď	B59147	TX5
4	167	ö	67	7	E59147	Tx5.2
Ŋ	148	4.	63	7	C59147	Gm5.1
9	129.5	•	62	7	G59147	Im5.1
7	63	•	423	7	B89784	cal pro
80	62		715	7	S77439	
σ	61	æ	315	Н	HNVZVT	hemagglutinin prec
10		8	389	~	H90413	conserved hypothet
11	59.5		457	7	T18347	gag protein homolo
12	9	18.0	2148	Н	A56081	insulin receptor -
13	59	7	111	~	T03701	SARB.2e protein. T
14	58	7.	551	7	AI1093	tide ABC
15	58	7.	929	~	A32495	Ç.
16	28		1126	7	ᅼ	DNA mismatch repai
17	28	7	1131	01	T38744	hypothetical prote
18	28	•	1992	Н	S02771	>
19	7	17.4	188	~	T48200	
20	57.5	17.4	541	7	T47290	-
21	~	•	772	7	H84605	Н
22	~	17.4	802	Н		
23	57	•	323	~	I64240	hypothetical prote
24	57		453	7	B97738	
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26	26		369	~	₹#	ות
27	26		3	~	2749	. –
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29	55.5		9	~	9463	cal prot

hypothetical prote	aldehyde oxidase (	viral mRNA transla	con-of-compalant	Son-or-seventess-2	2S albumin 2 precu	vomeronasal secret	probable exported	oxidoreductase Ci0	indoleacetamide hy	hypothetical prote	topoisomerase IV c	hypothetical prote	25 seed storage pr	Lola-like protein	Munc13-1 - rat	hymotherical prote
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518 2	907 1	1287 2 8	1297	7 /671 0.01	170 1 1	185 2	281 2	311 2	5 16.6 467 1	633 2	789 2	914 2	162 2	16.5 1010 2	1735 2 1	260 2 1

## ALIGNMENTS

RESULT 1

F59147
conotoxin P5.1 precursor - cone shell (Conus purpurascens)
N; Contains: conotoxin psa
C; Species: Conus purpurascens (purple cone)
C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 19-May-2000
C; Accession: F59147
R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan. M.B.; Cruz. L.J.; Hooner, D., Sherty
J. Biol. Chem. 274, 30664-30671, 1999
A, Title: The T-superfamily of conotoxins.
A; Reference number: A59147; MUID: 99452958; PMID: 10521453
A; Accession: F59147
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA; protein
A;Residues: 1-63 <wal></wal>
A; Cross-references: GB: AF167168; NID: q6103614; PIDN: AAF03688 1; PTD: q6103615
A;Note: submitted to GenBank, July 1999
C;Superfamily: unassigned conotoxins
C; Keywords: amidated carboxyl end; toxin; venom
F:1-22/Domain: signal sequence #status predicted <sig></sig>
F;23-50/Domain: propeptide #status predicted <pro></pro>
F;51-62/Product: conotoxin p5a #status experimental <mat></mat>
F;52-59,53-60/Disulfide bonds: #status experimental
F;62/Modified site: amidated carboxyl end (Leu) (amide in mature form from following gly
Ouerv Match 56 8%. Score 188. DB 2. Tendth 62.

. 0 Pred. No. 1.1e-15; 2; Mismatches 13; Indels Best Local Similarity 71.7%; Matches 38; Conservative

Gaps õ

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1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC 53 53 g

# RESULT 2

D59147

Conotoxin Gm5.2 precursor - cone shell (Conus gloriamaris)

C;Species: Conus gloriamaris (glory-of-the-sea cone)

C;Decies: Conus gloriamaris (glory-of-the-sea cone)

C;Dacession: D59147

R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty, B;Walker, C.S.; Steel, D.; Gonotoxins.

A;Title: The T-superfamily of conotoxins.

A;Reference number: A59147; MUID:99452958; PMID:10521453

A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA

A)Residues: 1-62 < WALD.

A)Cross-references: GB:AR167166; NID:g6103610; PIDN:AAF03686.1; PID:g6103611

A)Note: submitted to GenBank, July 1999
C)Superfamily: unassigned conotoxins
C)Superfamily: unassigned conotoxins
C)Keywords: amidated carboxyl end; toxin; venom

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31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSPECIES: Conns textile (cloth-of-gold cone)
C;Species: Steel, D; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty, J. Biol. Chem. 274, 30664-30671, 1999
A;Title: The T-superfamily of conotoxins.
A;Reference number: A59147; MUID:99452958; PMID:10521453
A;Title: The T-superfamily of conotoxins.
A;Reference number: A59147; MUID:99452958; PMID:10521453
A;Reference number: A59147; MUID:99452958; PMID:10521453
A;Reference number: A59147
A;Status: prelliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;References: GB:AFF57164; NID:g6103606; PIDN:AAF03684.1; PID:g6103607
A;Note: submitted to GenBank, July 1999
C;Superfamily: unassigned conotoxins
C;Superfamily: unassigned conotoxins
C;Superfamily: unassigned conotoxins
C;Superfamily: signal sequence #status predicted <RIO>
F;23-49/Domain: propeptide #status predicted <RIO>
F;20-57;Sl-58/Disulfide bonds: #status predicted <AMT>
F;50-57;Sl-58/Disulfide bonds: #status predicted
F;60-57;Sl-58/Disulfide bonds: #status predicted
F;60-757-751-78/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;pecies: Conus textile (cloth-of-gold cone)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Oct-2000
C;Date: 03-Dec-1999 #sequence_revision N.B.; Director, L.J.; Hooper, D.; Shetty
J. Blod. Chem. 274, 30664-30671, 1999
A;Title: The T-superfamily of conotoxins.
A;Recension: B59147
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-67 - (WAL)
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-67 - (WAL)
A;Cross-references: GB:AF167167; NID:g6103612; PIDN:AAF03687.1; PID:g6103613
A;Note: submitted to GenBank, July 1999; named tx5a in GenBank entry AF167167, release 1
B;Rigby, A.C.; Lucas-Meunier, E.; Kalume, D.E.; Czerwiec, E.; Hambe, B.; Dahlqvist, I.; Proc. Natl. Acad. Sci. U.S.A. 96, 5758-5763, 1999
A;Title: A conotoxin from Conus textile with unusual posttranslational modifications red
A;Reference number: A59044; MUID:99254114; PMID:10318957
                                                                                                                                                               in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MCCLPVFVILLLLIASAPSVDAQPKTKDDVPLAPLHDNAKSALQ-HLNQRCCQTFYWC 57
                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRCLPVFVILLLLIASAPSVDAQPKTKDDVPLAPLHDNIRSTLQTLR-KKVCC
                                                                                                                                                                                                                                                                                                                                                                                                       1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conotoxin Tx5.2 precursor [validated] - cone shell (Conus textile) N;Alternate names: epsilon-conotoxin TxIX N;Contains: conotoxin Tx5a
                                                                                                                                                                                                                                            Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                         10; Indels
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-49/Domain: propeptide #status predicted <PRO>F;50-60/Product: conotoxin gm5 #status predicted <MAT>F;50-60/Product: conotoxin gm5 #status predicted <AMT>F;51-58,52-59/Disulfide bonds: #status predicted F;60/Modified site: amidated carboxyl end (Ser) (amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                DB 2;
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Pred. No. 1.8e-13;
5; Mismatches 15
                                                                                                                                                                                                                                        54.5%; Score 180.5; DB 2 71.7%; Pred. No. 8.5e-15; ive 4; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 51.2%;
Local Similarity 63.8%;
les 37; Conservative
                                                                                                                                                                                                                                                                                                                              38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: A59044
A, Status: preliminary
A, Molecule type: protein
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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C.Comment: This conoctoxin reduces both presynaptic calcium influx and acetylcholine relectionment: This conoctoxin reduces both presynaptic calcium influx and acetylcholine relections are signed conotoxins circle structured caid; glycoprotein; hydroxyproline; toxin; venom F;1-19/Domain: signal sequence #status predicted <5RG>
F;20-50/Domain: signal sequence #status predicted <PRO>
F;21-63/Product: conotoxin tx5a #status experimental <ART>
F;44-64/Domain: carboxyl-terminal propeptide #status predicted <CRP>
F;51,54/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F;51,59/Domain: are semental carboxyglutamic acid (Glu) #status experimental
F;51,50/Domain: Carboxyl-terminal first minal propeptide #status experimental
F;60/Binding site: carbohydrate (Thr) #status experimental
F;60/Binding site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conotoxin Gm5.1 precursor - cone shell (Conus gloriamaris)
C.Species: Conus gloriamaris (glory-of-the-sea cone)
C.Species: Conus gloriamaris (glory-of-the-sea cone)
C.Accession: C59147
R.Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty A.Tile: The T-superfamily of conotoxins.
A.Title: The T-superfamily of conotoxins.
A.Reference number: A59147; MUID:99452958; PMID:10521453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condoxaxin ins.; precursor, come such (Concordants)
condoxaxin ins.; precursor, concordants (inperial cone)
C;Species: Comus imperialis (inperial cone)
C;Species: Comus imperialis (inperial cone)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000
C;Accession: G59147
R;Walker, C. S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.;
J. Biol. Chem. 274, 30664-30671, 1999
A;Title: The T-superfamily of conotoxins.
A;Reference number: A59147; MUID:99452958; PMID:10521453
A;Accession: G59147
A;Accession: G59147
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-62 <WAL>
A;Cross-references: GB:AF167169; NID:g6103616; PIDN:AAF03689.1; PID:g6103617
A;Mote: submitted to GenBank, July 1999
C;Superfamily: unassigned conotoxins
C;Keywords: amidated carboxyl end; toxin; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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A;Note: submitted to GenBank, July 1999
C;Superfamily: unassigned conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 167; DB 2; Length 67;
Pred. No. 4e-13;
1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 148; DB 2; Length 63;
Pred. No. 7.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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F)51-63/Product: concloxin gm5 #status predicted <MAT>F)51-63/Product: concloxin gm5 #status predicted <MAT>F)52-59,53-60/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.5%;
62.3%;
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hemagglutinin precursor - vaccinia virus (strain Tiantan)
C;Species: vaccinia virus
C;Accession: JL0108
R;Jin, D.; Li, Z.; Jin, Q.; Yuwen, H.; Hou, Y.
J. Exp. Med. 170, 571-576, 1989
A;Title: Vaccinia virus hemagglutinin. A novel member of the immunoglobulin superfamily. A;Title: Vaccinia virus hemagglutinin. A novel member of the immunoglobulin superfamily. Ascession: JL0108, MUID:89328331; PMID:2754392
A;Reference number: JL0108, MUID:89328331; PMID:2754392
A;Residues: 1-315 * valus
A;Residues: 1-315 * valus
A;Residues: 1-315 * valus
A;Cross-references: GB:X15709; GB:MS7773; NID:g61313; PIDN:CAA33740.1; PID:g61314
C;Superfamily: vaccinia virus hemagglutinin; immunoglobulin homology
C;Keywords: glycoprotein; hemagglutinin; late protein; transmembrane protein
F;17-15/Domain: signal sequence #status predicted <MGG-
F;27-105/Domain: immunoglobulin homology </td>

F;27-105/Domain: immunoglobulin homology 

F;280-302/Domain: inmunoglobulin homology 

F;280-302/Domain: inmunoglobulin homology 

F;30-315/Domain: intracellular #status predicted <TMM>F;30-315/Domain: intracellular #status predicted <INT>F;37,69,112,161,254/Binding site: carbohydrate (Asn) (covalent) #status predicted

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gag protein homolog, truncated - rice blast fungus magnaporthe gypsy retrotransposon C;Species: Magnaporthe grisea (rice blast fungus) C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C;Accession: T18347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE006641; NID: 913815727; PIDN: AAK42567.1; GSPDB: GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                --NAKSTLQRHQDKSVCCGYKLCFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 1; Length 315;
Pred. No. 11;
5; Mismatches 18; Indels
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Pred. No. 18;
3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 PSVDARLKTKDDVPLSSFRDNAKSTLQRHQDK 49
                                             20 VDARLKTKDDVPLSSFRD---
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39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.1%;
46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.4
Best Local Similarity 39.5
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 46.9
nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: H90413
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Matches
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F;1-19/Domain: signal sequence #status predicted <SIG>
$20-45/Domain: propeptide #status predicted <PRO>
F;46-60/Product: conoctoxin im5 #status predicted <MAT>
F;50-57,51-58/Disulfide bonds: #status predicted
F;60/Modified site: amidated carboxyl end (Trp) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: 877439
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-715 <KAN>
A;Residues: 1-715 <KAN>
A;Cross-references: EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BAA17286.1; PID:d101801
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: B89784
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: BA000018; PID: 913700130; PIDN: BAB41429.1; GSPDB: GN00149
                                                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A,Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein SA0207 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                 1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKL-CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein slr1135 - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                        DB 2; Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 2; Length 715;
Pred. No. 18;
7; Mismatches 21; Indels
                                                                                                                                                                                                                              23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRCLPVFVILLLL-TASGPSVDARLKTKDDVPLSSFRDNAK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S77439
                                                                                                                                                                        Score 129.5; DB 2
Pred. No. 1.3e-08;
5; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.0%; Score 63; DB 2; 31.7%; Pred. No. 8.6; cive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: maltose-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain N315
                                                                                                                                                                        39.1%;
50.8%;
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l Similarity 28.0%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.7*
Matches 13; Conservative
                                                                                                                                                                                               Best Local Similarity 50.8 Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-423 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                           PCG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PWG 61
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C,Accession: T03701
R;Ward, E.R.; Uknes S.J.; Williams, S.C.; Dincher, S.S.; Wiederhold, D.L.; Alexander, D Plant Cell 3, 1085-1094, 1991
A;Title: Coordinate gene activity in response to agents that induce systemic acquired replacement number: Z15021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligopeptide ABC transporter-binding protein homolog lmo0152 [imported] - Listeria monoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: Al1093
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
D; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma, A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Waitournam, A.; Ma, A; Title: Comparative genomics of Listeria species.
A; Ritle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rep-1 protein, form A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Feb-1997
C;Accession: A33495; A30939
R;Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-551 <CLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98367.1; PID:g16409511; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2001
                                                                                                                                                                                                     C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RCLPVFVIL - - LLLTASGPSVDARLKTXDDVPLSSFRDNAKSTLQRHQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 2; Length 551;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:M97362; NID:g170340; PID:g170341
C;Genetics:
A;Gene: SAR8.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-111 <WAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.8%; Score 5., 20.8%; Pred. No. 7.7; +ive 19; Mismatches
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                                                                                                                                                          SAR8.2e protein, TMV-inducible - common tobacco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | |::| |
ICPCKYQICSKC 78
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin receptor - fruit fly (Drosophila melanogaster)
N;Contains: protein-tyrosine kinase (EC 2.7.1.-)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Bate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A56081; A26378; A24147
C;Date: 10-Sep-1999 #sequence receptor contains a novel carboxyl-terminal extension 15
B;Ruan, Y; Chen, C; Cao, Y; Garofalo, R.S.
J; Biol. Chem. 270, 4236-4243, 1995
A;Title: The Drosophila insulin receptor contains a novel carboxyl-terminal extension 15
A;Reterace number: A56081; MUID:95181404; PMID:7876183
A;Accession: A55081
A;Retais: preliminary; not compared with conceptual translation
A;Residues: 1-2148 cRUA>
A;Residues: 1-2148 cRUA>
A;Residues: 1-2148 cRUA>
A;Residues: 1-2148 cRUA>
A;Coss-references: GB:U18351
B;Ochem. Biophys. Res. Commun. 141, 474-481, 1986
A;Title: Cloning of a Drosophila cDNA encoding a polypeptide similar to the human insuli
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A;Molecule type: mRNA
A;Molecule type: mN14778; MID:9157759; PIDM:AAA28644.1; PID:9157760
A;Cross-references: GB:M14778; MID:9157759; PIDM:AAA28644.1; PID:9157760
B;Petruzzelli, L; Herrerar, R; Arenas-Garcia, R; Fernandez, R; Birnbaum, M.J; Rosen, Proc. Natl. Acad. Sci. U.S.A. 83, 47104714; 1986
A;Title: Isolation of a Drosophila genomic sequence homologous to the kinase domain of the control of the control type to the control t
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R;Farman, M.L.; Tosa, Y.; Nitta, N.; Leong, S.A.
Mol. Gen. Genet. 251, 665-674, 1996
A;Title: MAGGY, a retrotransposon in the genome of the rice blast fungus Magnaporthe gri
A;Reference number: Z18882; MUID:96335141; PMID:8757397
A;Accession: T18347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-457 <FAR>A;Cross-references: EMBL:L35053; NID:g522300; PID:g522301; PIDN:AAA33419.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 'L10Q',1308-1476,' DGHDDVS',1484-1522,' PF',1525-1572,' QAWCLLLVPVT',1583-1594,
A; Residues: 'L10Q',1308-1476,' DGHDDVS',1484-1522,' PF',1525-1572,' QAWCLLLVPVT',1583-1594,
A; Cross-references: GB:M13568; NID:g157761; PIDN:AA28645.1; PID:g157762
A; Experimental source: unspecified Drosophila species
A; Genetics:
A; Gene: FlyBase: INR
A; Cross-references: FlyBase: PBgn0013984
C; Superfamily: Drosophila insulin receptor; protein kinase homology
C; Reywords: ATP; glycoprotein; hormone receptor; kinase-related transforming protein; p}
P; 1315-1331/pomain: transmembrane #steuus predicted <a href="https://www.mcde.com/mb.arc/">mcde.com/mase-related transforming protein; p}</a>
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C;Superfamily: Drosophila insulin receptor; protein kinase homology
C;Superfamily: Drosophila insulin receptor; kinase-related transforming protein;
C;Reywords: AFP; glycoprotein; hormone receptor; kinase-related transforming protein;
F;1115-1331/Domain: transmembrane #status predicted <TMM>
F;1373-1661/Domain: protein kinase homology <KIN>
F;1381-1389/Region: protein kinase AFP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.0%; Score 59.5; DB 2; Length 4 28.1%; Pred. No. 24; tive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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. 1e+02;
22;
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A;Mobile element: magnaporthe gypsy retrotransposon
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26.8%; Pred. No. 1e+0:
:ive 12; Mismatches
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Best Local Similarity 28.19
Matches 16; Conservative
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Mol. Cell. Biol. 9, 3058-3072, 1989
A;Title: Dual bidirectional promoters at the mouse dhfr locus: cloning and characterizat A;Title: Dual bidirectional promoters at the mouse dhfr locus: cloning and characterizat A;Reference number: A32495, MUD:89384567; PMID:2674679
A;Residon: A32495
A;Residon: A32495
A;Residone: L-929 <LIN>A;Residones: L-929 <LIN>A;Residones: L-929 <LIN>A;Residones: L-929 <LIN>A;Residones: L-929 <LIN>A;Residones: L-920 <LIN>A;Residones: L-920 <LIN>A;Residones: L-920 <LIN>A;Residones: C;Rendidones: C;Reywords: DNA binding
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Query Match
Best Local Similarity 32.1%; Pred. No. 71;
Matches 18; Conservative 5; Mismatches 17; Indels 16; Gaps

3;

ò QQ Search completed: August 10, 2004, 16:04:56 Job time : 19.2703 secs

Many Silled

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 10, 2004, 15:56:10 ; Search time 13.4054 Seconds (without alignments) 240.824 Million cell updates/sec Run on:

331 1 MRCLPVFVILLLLTASGPSV.....LQRHQDKSVCCGYKLCFPCG US-10-072-602B-352 Title: Perfect score: Sequence:

62

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0
Maximum DB seq length: 2000000000

141681

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P47769 Q01206 Q01206 P13517 Q60857 Q45347 Q10369 P07983 P480665 Q81pb4
RPOC_MYCTU POLI BAYMJ CAPB_YEAST THSB_ARCFU S6A4_MOUSE INSR_DROME IRED_BACPA IRED_BACPA GUNI_BACSU S6AC_HUMAN PSKR_DAUCA
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### ALIGNMENTS

SEQUENCE OF 49-61, AND MASS SPECTROMETRY.

MEDLINE=20564325; PubMed=10988292; Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H.;

"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Comus marmoreus.";
J. Biol. Chem. 275:39516-39522 (2000). 

SEQUENCE OF 49-61, SYNTHESIS, MASS SPECTROMETRY, AND STRUCTURE BY NMR. TIŠSUB=Venom;
MEDLINE=21419681; PubMed=11528421;
Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,

"Two new classes of conopeptides inhibit the alphal-adrenoceptor and noradrenaline transporter.";

Nat. Neurosi. 4:902-907(2001).

-!- FUNCTION: Inhibits the neuronal noradrenaline transporter.

-!- SUBCELIULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed by the venom duct.

-!- PTM: Exists in two forms, due to cis-trans isomerization at His-Lewis R.J.;

59-Hyp-60.

-i- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.

InterPro; IPR004214; Conctoxin.

Pfam; PF02926; Conoctoxin; 1.

Neurotoxin; Toxin; Hydroxylation; Signal.

SIGNAL

19 POTENTIAL.

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Gaps

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Length 63;

53 53

62 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J., Walker C.S., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M., Bandyopadhyay P., Craig A.G., Olivera B.M.; J. Biol. Chem. 274:36030(1999).

-: FUNCTION: Not known. Has only been studied at nucleotidic level...
-: SUBCELLULAR LOCATION: Secreted...
-: TISSUE SPECIFICITY: Expressed by the venom duct...
-: SIMILARITY: Belongs to the conotoxin T-superfamily.
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BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-61 PROVIDE AMIDE GROUP)
                                                    AMIDATION (G-63 PROVIDE AMIDE GROUP).
                                                                                                                                                                                    1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Venom duct;

MEDLINES-9945-958; PubMed=10521453;

MEDLINES-9945-958; PubMed=10521453;

Malker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,

Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,

Handyopadhyap, P., Craig A.G., Olivera B.M.;

"The T-superfamily of conotoxins.";

J. Biol. Chem. 274:30664-30671(1999).
                                                                                                                                                                                                                         1 MRCLPVFVILLLIPSAPCVDAHPKTKDDMPLASFHDNAKGTLQRFWKKRGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 180.5; DB 1; Length 62;
Pred. No. 5.9e-16;
4; Mismatches 10; Indels
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Ututative conocoxin GMS.2 precursor.
Conus gloriamaris (Glory of the sea).
Eukaryota, Metazoa, Mollusca; Gactropoda; Orthogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
6C8C0ADB810732C9 CRC64;
                                                                      82A28478C13D7EA9 CRC64;
                                                                                                          Score 188; DB 1;
Pred. No. 6.8e-17;
2; Mismatches 13,
                                                                                                                                                                                                                                                                                                                                                                 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 43, Last annotation update)
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CONOTOXIN P5A.
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Pfam; PF02950; Conotoxin; 1.
Toxin; Signal; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF167166; AAF03686.1; -.
PIR; D59147; D59147.
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Best Local Similarity 71.7%;
Matches 38; Conservative
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Best Local Similarity 71.7
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=37336;
  51
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63 AA;
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Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
Bandyopadhyay P., Craid A.G., Olivera B.M.;
J. Biol. Chem. 274:36030-36030(1939)
- FUNCTION: Low levels of the peptide injected into male specimens
- FUNCTION: Low levels of the peptide injected into male specimens
- of the Siamese fighting fish causes an immediate aggressive
diaplay in this fish in response to their reflection when placed
in a mirrored aguarium; High levels of the peptide suppressed this
- behavior. No effect is observed when injected into mice.
- SINELLIGIAR LOCATION: Secreted.
- TISSUE SPECIFICITY: Expressed by the venom duct.
- MASS SPECIFROMETRY: MM=1337.5; METHOD=LSIMS.
- SIMILARITY: Belongs to the conotoxin T-superfamily.
                                                                                                                                                                                                 1 MRCLPVFVILLLITASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J., Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M., Bandyopadhyap P., Craig A.G., Olivera B.M.; "The T-superfamily of conotoxins."; J. Biol. Chem. 274:30664-30671(1999).
                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens (Purple cone).
Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., SEQUENCE OF 51-62, MASS SPECTROMETRY, AND
                                                                                                                          Length 61;
                                                                                                                                                              19; Indels
          LAMBDA-CONOTOXIN CMRVIB.
                                                                  HYDROXYLATION.
F4DE5B5A97EB8DBA CRC64;
                                                                                                                            Score 191; DB 1;
Pred. No. 2.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    63 AA
                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom, and Venom duct;
MEDLINE=99452958; PubMed=10521453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF167168; AAF03688.1; -.
PIR; F59147; F59147.
InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02950; Conotoxin; 1.
              61
61
58
60
6499 MW;
                                                                                                                            57.7%;
62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin, Amidation, Signal.
SIGNAL 1 19
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conotoxin p5a precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                Similarity 38; Conserv
              49
52
53
60
61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                       61 C 61
                                                                                                                                                                                                                                                                                                                         C 61
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              PEPTIDE
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DISULFID
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                                                                                                                                Query Match
                                                                                      SEQUENCE
                                                                                                                                                    Local
                                                                          MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                      CONPU
                                                                                                                                                                        Matches
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Gaps

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Conus textile (Cloth-of-gold cone).

Bukaryota; Metazoa, Mollusca; Gaetropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                  TISSUE=Venom, and Venom duct;
MEDLINE=99452958; PubMed=10521453;
Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
Bandyopadhyay P., Craig A.G., Olivera B.M.;
"The T-superfamily of conotoxins.";
J. Biol. Chem. 274:30664-30671(1999).
                                                                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 51-63, AND MASS SPECTROMETRY TISSUE=Venom, and Venom duct;
          30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Epsilon-conotoxin TXIX precursor (Conotoxin tx5a).
                                                                                                                   NCBI_TaxID=6494;
 P81755; Q9U6Z7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ı;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58
                                                                                                                                                                                                                                                                                                                                                                              Malker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
Bandyopadhyay P., Craig A.G., Olivera B.M.;
J. Biol. Chem. 274-33603-460301999).
-!- FUNCTION: Not known. Has only been studied at nucleotidic level.
-! SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin T-superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
         23
                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
PUTATIVE CONOTOXIN TXS.1.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-61 PROVIDE AMIDE GROUP)
  1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                 Putative conotoxin TX5.1 precursor.
Conus textile (Cloth-of-gold cone).
Eukaryota; Metazaa, Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                               TISSUE=Venom duct;
MEDLINE=99452958; PubMed=10521453;
Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
Bandyopadhyay P., Craig A.G., Olivera B.M.;
"The T.superfamily of conctoxins.";
"The T.superfamily of conctoxins.";
J. Biol. Chem. 274:30664-30671(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 62;
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CE29803DEB0DA421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.4e-14; 5; Mismatches 15
                                                                                                                                  (Rel. 41, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                               62 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 169.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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InterPro; IPR004214, Conotoxin,
Pfam; PF02950; Conotoxin; 1.
Toxin; Signal; Amidation.
                                                                                                                   28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF167164; AAF03684.1; -.
PIR; BS9147; BS9147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AA; 6857 MW;
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 63.8
les 37; Conservative
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=6494;
                                                                                                                                              15-MAR-2004
                                                                                                                                  28-FEB-2003
                                                                                           CONTE
                                                                                          CX51 CON
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MOD_RES
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Matches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                "Mechanisms for evolving hypervariability: the case of conopeptides.";
Mol. Biol. Evol. 18:120-131(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 51-63, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY

    J. Mass Spectrom. 35:145-156 (2000).
    J. Mass Spectrom. 35:145-156 (2000).
    FUNCTION: Acts at presynaptic membranes, blocking the calcium channels. Causes hyperactivity upon intracranial injection into mice. Causes dorsal fins drooping in fish.
    SUBCELLULAR LOCATION: Secreted.
    TISSUE SPECIFICITY: Expressed by the venom duct.
    PTM: O-glycan consists of the disaccharide Gal-GalNac.
    MASS SPECTROMETRY: MW=1929.4; METHOD=Electrospray.
    MASS SPECTROMETRY: MW=1929.4; METHOD=MASS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure determination of two conotoxins from Conus textile by combination of matrix-assisted laser desorption/ionization time-of-flight and electrospray ionization mass spectrometry and blochemical methods."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=99254114; PubMed=10318957;
Rigby A.C., Lucas-Meunier E., Kalume D.E., Czerwiec E., Hambe E Dahlqvist I., Fossier P., Baux G., Roepstorff P., Baleja J.D., Furie B.C., Furie B., Stenflo J.D., "A conotoxin from Couns textile with unusual posttranslational modifications reduces presynaptic Ca2+ influx.", proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).
Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J., Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M., Bandyopadhyay P., Craig 4.G., Olivera B.M.; J. Biol. Chem. 274:36030-36030(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20146306; PubMed=10679974;
Kalume D.B., Stenflo J.P., Czerwiec E., Hambe B., Furie B.C.,
Furie B., Roepstorff P.;
                                                                                                                                                                                                                                                                                                                              Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 51-63, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                           MEDLINE=21105969; PubMed=11158371;
                                                                                                                                                                                                                                                             duct;
                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                     TISSUE=Venom
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67 AA.

PRT;

STANDARD;

RESULT 5 CXET\_CONTE ID \_CXET\_CONTE

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CONIM
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PEPTIDE
DISULFID
DISULFID
                                                                                                                                  Query Match
Best Local S:
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                                                                                            DISULFID
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                                                                       PROPEP
                                                           SIGNAL
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                                                                                                                                                         Matches
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-I. FUNCTION: Not known. Has only been studied at nucleotidic level.

-I. SUBCELLULAR LOCATION: Secreted.

-I. TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                            Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;
                                                                                                                                                                                                                                                                               Gaps
                                                                       Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor; Vitamin K; Signal;
                                                                                                                                                                                                                                                                                                  1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                                                                                                                                                                                                                                                                                                                1 MRCFPVFIILLLIASAPCFDARTKTDDDVPLSSLRDNLKRTIRTRLMIRECC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=37336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99452958; PubMed=10521453; Malker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J., Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M., Bandyopadhyay P., Craig A.G., Olivera B.M.; "The T-superfamily of conotoxins."; J. Biol. Chem. 274:30664-30671(1999).
                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
Putative conotoxin Gall precursor.
Conus gloriamaris (Glory of the sea).
Eukaryota; Metazoa; Mollusca; Gastropoda;
                                                                                                                                                                                                                                                         Score 167; DB 1; Length 67; Pred. No. 3.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: Belongs to the conotoxin T-superfamily.
                                                                                                                                                                                 GAMMA-CARBOXYGLUTAMIC ACID. GAMMA-CARBOXYGLUTAMIC ACID. BROMINATION.
                                                                                                                                                                                                               HYDROXYLATION.
O-LINKED (GALNAC. ..).
7270505504D6BB3D CRC64;
                                                                                                                                         EPSILON-CONOTOXIN TXIX
                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                              63 AA
                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                    POTENTIAL
                                            PDB; 1WCT; 08-JUN-99.
InterPro; IPR004214; Conotoxin.
      EMBL; AF167167; AAF03687.1; -.
                                                                                                                                                                                                                                                         Query Match 50.5%;
Best Local Similarity 62.3%;
Matches 33; Conservative
                       AF214958; AAG60386.1;
                                                                                                                                                                                                                                      7587 MW;
                                                                Pfam, PF02950; Conotoxin; 1
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                      119
63
63
53
53
63
63
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                                 PIR; E59147; E59147
                                                                                                                                                                                                                                       67 AA;
                                                                                                                             20
51
52
53
53
63
63
                                                                                                            3D-structure
                                                                                                                                                                                                                                                                                                                                                                              CONGL
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                                                                                                                                                              DISULFID
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PROPEP
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                                                                                                                   SIGNAL
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CONGL
                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J., Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M., Bandyopadhyay P., Craig A.G., Olivera B.M.; Bandyopadhyay P., Craig A.G., Olivera B.M.; J. Biol. Chem. 274:36030-36030(1999).
-: FUNCTION: Not known. Has only been studied at nucleotidic level.-: STUBCELLIARAR LOCATION: Secreted.
-: STUBCELLIARAR LOCATION: Secreted.
-: TISSUB SPECIFICITY: Expressed by the venom duct.
-: SIMILARITY: Belongs to the conotoxin T-superfamily.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Venom duct;

MEDLINE=9945-2958; PubMed=10521453;

MEDLINE=945-2958; D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,

Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,

Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,

Bandyopadhyap, P., Craig A.G., Olivera B.M.;

"The T-superfamily of conotoxins.";

J. Biol. Chem. 274:30664-30671(1999).
                                                                                                                                                                                                                                                                                                                                                                                                           1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                                                                                                                                                                                                                                                                                                          Score 148; DB 1; Length 63; Pred. No. 7.4e-12;
                                                                                                                                                                                                                                                                                                                                                           15; Indels
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PUTATIVE CONOTOXIN IM5.1.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                      BY SIMILARITY.
PUTATIVE CONOTOXIN GM5.1.
                                                                                                                                                                                                                                                          00B24439E5DDE272 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AA
                                                                                                                                                                                                                                                                                                                                     Pred. No. 7.4e
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                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative conotoxin Im5.1 precursor. Conus imperialis (Imperial cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR, G59147; G59147.
InterPro: IPR04014; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
Toxin; Signal; Amidation.
EMBL; AF167165; AAF03685.1; -.. PIR; C59147; C59147. InterPror; IPR004214; Conotoxin. Pfam; PF02950; Conotoxin; 1. Toxin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF167169; AAF03689.1; -.
                                                                                                                                                                                                                                                                                                                44.7%;
58.5%;
                                                                                                                                                                                                                                                               7398 MW;
                                                                                                                                                                                                                                                                                                                                        Local Similarity 58.5
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=35631;
                                                                                                                                                                                                                                                               63 AA;
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449
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Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
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                                                                                                                                                                            Lewis R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VACCT
                [1]
SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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P16561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
HEMA_VACCT
                REPRESENTATION OF COLOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
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                                                                                                                                                                                                                                                1 MRCLPVFVILLLITASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKL-CF
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H.; "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
AMIDATION (G-61 PROVIDE AMIDE GROUP)
                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
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Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Meogastropoda; Conoidea; Conidae; Conus.
                                                                                                           Score 129.5; DB 1; Length 62; Pred. No. 1.5e-09;
                                                                                                                                                                   23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 1; Length 11;
Pred. No. 0.013;
0; Mismatches 1; Indels
                            (BY SIMILARITY).
9570E7C02275796D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROXYLATION.
277AAC60B7232B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CXLI CONMR
P58807;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lambda/chi-conotoxin MrIB (Chi-MrIB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AA.
                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20564325; PubMed=10988292;
                                                                                                           39.1%;
50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.5%;
90.9%;
                                                     7030 MW;
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                                                                                             Query Match
Best Local Similarity 50.8'
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                     62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=42752;
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09
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                                                                                                                                                                                                                                                                                                                                                                            59 PWG 61
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                                                SEQUENCE
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MOD_RES
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ID CXLL C
PS 80 FEB 1
DT 28 - FEB 1
DE Lambda 2
OC EUMARY
OC BUKARY
OC BUKA
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                                                                                                                                                                               "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
                                                                                                                                                                                                            noradrenaline transporter.";
Nat. Neurosi. 4:902-907(2001).
-!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- PTM: Exists in two forms, due to cis-trans isomerization at His-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=89328331; PubMed=2754392;
Dongyan J., Zhiliang L., Qi J., Hao Y., Yunde H.;
"Vaccinia virus hemagglutinin. A novel member of the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinia virus (strain Tian Tan).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superfamily.";
J. Exp. Med. 170:571-576(1989).
-!- SUBCELULAR LOCATION: Type I membrane protein.
-!- PTM: Glycosylated; contains phosphate and sulfate-substituted
glycans. O-glycosylation is required for hemagglutination and
hemadsorption activities of infected cell membranes.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                    MEDLINE=21419681, PubMed=11528421,
Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
Atkins A., Palant B., Craik D.J., Adams D.J., Alewood P.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family PDB; 11EO; 03-APR-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 1; Length 13;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      11-Hyp-12.
-!- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROXYLATION.
277AAC376EAD2B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotoxin; Toxin; Hydroxylation; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
SYNTHESIS, AND STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.5%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 10
12 12
13 AA; 1382 MW;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hemagglutinin precursor.
HA OR A56R.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              MSH3 MOUSE
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SUBCELLULAR LOCATION: FOUND IN THE CYTOPLASM IN UNSTIMULATED CELLS
BUT S TRANSLOCATED TO THE MEMBRANE RUFFLES IN CELLS STIMULATED
TISSUE SPECIFICITY: Brain and interlimb region.

TISSUE SPECIFICITY: Brain and interlimb region.

DEVELOPMENTAL STAGE: At the 4- to 5-somite stage (4/5S) found in DEVELOPMENTAL STAGE: At the 4- to 5-somite stage (4/5S) found in the embryo in scattered cells across the neural plate in the presumptive mid/ hindbrain region. At 7/8S found in the isthmus and throughout the presumptive r1 territory. Between 10-14S stage found throughout the R1 region and at the isthmic constriction. By 26S the anterior limit of expression extends into the posterior midbrain region and this pattern of expression is maintained at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minowada G., Jarvis L.A., Chi C.L., Neubuser A., Sun X., Hacohen N., Krasnow M.A., Martin G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Vertebrate sprouty genes are induced by FGF signaling and can cause
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Cell. Neurosci. 15:22-35(2000).
-!- FUNCTION: May play an important role in FGF-mediated patterning the mid/hindbrain region by acting to modulate the signaling efects of FGF8 through participation in a regulatory negative
            Hemagglutinin; Envelope protein; Late protein; Glycoprotein; Signal;
Transmembrane; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chambers D., Medhurst A.D., Walsh F.S., Price J., Mason I.; Dibfferential display of genes expressed at the midbrain-hindbrain junction identifies sprouty2: an FGF8-inducible member of a family intracellular FGF antagonists.";
                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                            (POTENTIAL) .
                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                   18.4%; Score 61; DB 1; Length 315; 39.5%; Pred. No. 3.7;
                                                                                                                                                                                                                                                           18; Indels
                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                         E049448640879FF4 CRC64;
                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                   (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
                                                                                                                                                                                                                                                                                        1 MRCLPVFVILLLITASGPSVDARLKTKDDVPLSSFRDN 38
                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                            (GLCNAC
                                                                                                                                                                                                                                              Pred. No. 3.7;
5; Mismatches
                                                                                                            IG-LIKE V-TYPE.
                                                         HEMAGGLUTININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chondrodysplasia when overexpressed.";
Development 126:4465-4475(1999).
                                                                                                                                                                N-LINKED
N-LINKED
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                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=99429807; PubMed=10498682;
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MEDLINE=20130796; PubMed=10662503;
                                                                                                                                                                                                          34772 MW;
  PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2004 (Rel. 43, Last a Sprouty homolog 2 (Spry-2).
                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
                                                      315
279
303
315
121
103
37
69
                                                                                                                                                                               161
254
315 AA;
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                   17
280
304
17
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                                                                                                                                                                                                                                                                                                                                                                                       CHICK
                                                       CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                      Query Match
                                                                                                                          DISULFID
                                                                                                                                         CARBOHYD
                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                    Q9PTLZ;
                                                                                               DOMAIN
                                                                                                               DOMAIN
                                             SIGNAL
                                                                                                                                                                                                                                                              Matches
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later stages

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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
-!- INDUCTION: By FGF signaling.
-!- DOMAIN: The Cys-rich domain is responsible for the localization of the protein to the membrane ruffles.
-!- SIMILARITY: Belongs to the sprouty family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu K., Niu L., Linton J.P., Crouse G.F., "Characterization of the mouse Rep-3 gene: sequence similarities to bacterial and yeast mismatch-repair proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89384567; PubMed=2674679; Linton J.P., Yen J.-Y.J., Selby E., Chen Z., Chinsky J.M., Liu K., Kellems R.E., Crouse G.F.; "Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization of two mRNA classes of the divergently transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell. Biol. 9:3058-3072(1989).
FUNCTION: NOT KNOWN. PROBABLE DNA-REPAIR PROTEIN.
SIMILARITY: Belongs to the DNA mismatch repair mutS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 LLLTASGPSVD--ARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DNA mismatch repair protein Msh3 (Repair-3 protein) (REP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 1; Length 313;
Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu K., Niu L., Linton J.P., Crouse G.F.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                               313 AA; 34417 MW; 614C335E0DC36E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1091 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=95011610; PubMed=7926796;
                                                                                                                                                                                                                                                                                                 EMBL; AF176904; AAD56005.1; -.
InterPro; IPR007875; Sprouty.
Pfam; PF05210; Sprouty; 1.
Developmental protein; Membrane.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.8%;
30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-917 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 30.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 147:169-177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Wonse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR REP-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSH3 MOUSE
P13705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rep-1 gene.
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PROSITE; PS01359; ZF_PHD_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z68144; CAA92265.1; -.
PIR; T38744; T38744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.5
Best Local Similarity 29.2
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799 IKNKDDVNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYSA CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 GPCPEVFOKTSDCKP---FNKRSKSVYTPLELQYLDMKQOHKDAVLCVECGYKYRF 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.5%; Score 58; DB 1; Length 1091;
32.1%; Pred. No. 34;
tive 5; Mismatches 17; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GPSVDARLKTKDDVPLSSFRDNAKSTL------ORHQDKSVC--CGYKLCF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1091 AA; 123074 MW; 822BF422436FD513 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
MV -> IL (IN REF. 2).
T -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein (3H1.12c in chromosome I.
SPAC3H1.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00466; DNA MISMATCH REPAIR 2; 1.
DNA repair; ATP-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                EMBL: L10313; AAB60711.1; JOINED. EMBL: L10314; AAB60711.1; JOINED. EMBL: L10315; AAB60711.1; JOINED. EMBL: L10316; AAB60711.1; JOINED. EMBL: L10316; AAB60711.1; JOINED. EMBL: L10318; AAB60711.1; JOINED. EMBL: M24919; AAA40051.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                   AAB60711.1; JOINED. AAB60711.1; JOINED. AAB60711.1; JOINED. AAB60711.1; JOINED.
                                                                                                                                                          AAB60711.1; JOINED.
AAB60711.1; JOINED.
AAB60711.1; JOINED.
                                                                                                                                                                                                JOINED.
                                                                                      AAB60711.1; JOINED AAB60711.1; JOINED
                                                                                                                                                                                                                                   AAB60711.1; JOINED.
AAB60711.1; JOINED.
AAB60711.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000432; MutS C.
InterPro; IPR000432; MutS C.
InterPro; IPR007860; MutS II.
InterPro; IPR007696; MutS II.
InterPro; IPR007695; MutS II.
Pfam; PF01624; MutS I; 1.
Pfam; PF01624; MutS I; 1.
Pfam; PF0188; MutS II; 1.
Pfam; PF00488; MutS II; 1.
ProDom; PD001263; MutS C; 1.
SWART; SM00534; MUTSac; 1.
                                                     AAB60711.1; (AAB60711.1;
                                                                                                                          AAB60711.1;
AAB60711.1;
                                                                                                                                                                                                                                 AAB60711.1;
                                                                                                                                                                                                                 AAB60711.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 32.19
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A32495; A32495.
MGD; MGI:109519; Msh3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                            EMBL; L10308; A
EMBL; L10309; A
EMBL; L10310; A
EMBL; L10311; A
EMBL; L10311; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                     L10296;
L10297;
                                                                                        L10298;
L10299;
                                                                                                                         110300;
                                                                                                                                             L10301;
                                                                                                                                                               L10304;
                                                                                                                                                                                              L10306;
                                                                                                                                                                                                                 L10307;
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Q10077;
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                                                                   EMBL;
EMBL;
EMBL;
EMBL;
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                                                                                                                                                                            EMBL;
EMBL;
EMBL;
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SO THE WAS READERS OF SERVICE SERVICES FOR SERVICES SERVI
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Registron Y. Peat N. Hayles J. Baker S., Basham D., Bowman S.,
R. Collins W. Combor P. Groni. And Colling Str. Charters C. M.,
R. Collins W. Combor P. Cornel. And Colling Str. Charters C. Wildman J. Charters S., Gable A., Hamilton W. Harris D. Hiddago J., France S.,
R. James K. Jones J. Hornby T., Waller B. McLes E., McChan J. S.,
R. James K. Jones S., Mandal K. Mandal K. McChan J. S.,
R. James K. Jones S., Mandal K. Mandal K. McChan J. S.,
R. James K. Jones S., Mandal K. McChan J. S.,
R. McCharter S., WcChear J. S.,
R. McCharter S., WcChear J. S.,
R. McCharter S., Sabap S.,
R. McCharter S., Sabap S.,
R. McCharter S., Sabap S.,
R. McCharter S., WcChear J. S.,
R. McCharter S., WcChear J., S.,
R. McCharter S., McChear J., S.,
R. McCharter S., McChear J., S.,
R. McCharter S., McChear J., S.,
R. McCharter S., R. McCharter S., WcChear S.,
R. McCharter S., R. McCharter S.,
R. M
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                                                                                                                                                                                                                                                                                                                                                  SUBDNIT: Muscle myosin is a hexameric protein that consists of 2 subunit: Muscle myosin is a hexameric protein that consists of 2 subunits wheavy chain subunits (MLC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2).

SUBGELIGIAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: The rodiike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.

MISCELANDOUS: Bach myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.elegans.
-!- MISCELLANEOUS: WHC A and WHC B are found exclusively in the body wall wascle. They co-assemble into body wall thick filament.
-!- SIMILARITY: Contains 1 myosin-like globular head domain.
-!- SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; rucess, smarr; SMART; SM0015; 10.
SMART; SM0015; 10.
PROSITE; PS50096; 1Q; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Multigene family.
ATP-binding; Methylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: There are four different myosin heavy chains in
                                                                    Dibb N.J., Maruyama I.N., Krause M., Karn J.; "Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene family."; J. Mol. Biol. 205:603-613 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN
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Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYLATION (TRI-) (POTENTIAL)
Y -> YVRKLKLFKKKINTIQKLNRLNFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1969 AA; 225509 MW; 64577BBAF7EAD80A CRC64;
                                                                                                                                                                                                                                                                 Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Muscle contraction.
-!- SUBUNIT: Muscle contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X08067; CAA30856.1; --
EMBL; Z78199; CAB01576.1; --
FDR; T236.2; S02771.
HSSP; P08799; INND.
HSSP; P08799; INND.
InterPro; IPR000048; IQ_region.
InterPro; IPR000048; IQ_region.
InterPro; IPR000409; Myosin_head.
InterPro; IPR00209; Myosin_head.
InterPro; IPR00201; IQ; IPR00201; IPR00201
                          STRAIN=Bristol N2;
MEDLINE=89178677; PubMed=2926820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subfragment (S2)
                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2;
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
NP BIND
DOMAIN
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1,

Gaps

5

21; Indels

12; Mismatches

Conservative

17.5%; 27.18;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + glycine = ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boucherie H., Dujardin G., Kermorgant M., Monribot C., Slonimski P.P.,
                                                                                                                                                                                                                                                   01_ARR-1988 (Rel. 07, Last sequence update)
15_MAR-2004 (Rel. 43, Last annotation update)
15_MAR-2004 (Rel. 43, Last annotation update)
16_MAR-2004 (Rel. 43, Last annotation update)
17_MAR-2004 (Rel. 43, Last annotation update)
18_MAR-2004 (Rel. 43, Last annotation update)
18_MAR-2004 (GARS) (Glycinamide
18_MAR-2004 (GARS) (Glycinamide
18_MAR-2004 (GARS) (Glycinamide
18_MAR-2004 (GARS) (ARR-2004 (GARS) (ARR-2004 (GARS) (GRS) (GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The Saccharomyces cerevisiae ADE5,7 protein is homologous to overlapping Drosophila melanogaster Gart polypeptides."; J. Mol. Biol. 190:519-528(1986).
                                  49
2 RCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fartmann B., Kramer B., Kramer W.;
Submitted (MAX-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                      802 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTR; A2643; A26343.
HSSP; P08178; ICLI.
Germonline; I41283; .
GO; GO:000573; ADES; 7.
GO; GO:0005737; C:Cytoplasm; IDA.
InterPro; IPR000728; AIR_Synth.
InterPro; IPR000115; Gars.
InterPro; IPR004733; PurM_cligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96093904; PubMed=7483834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=87061006; PubMed=3097325;
                                                                                                                                                                                                                                        (Rel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X04337; CAA27867.1; -. EMBL; Z72756; CAA96952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE OF 1-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00586; AIRS; 1.
                                                                                                                                                                                         STANDARD;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_mammal:*
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914460 09bpf5	O9BPF5	ç	5	1

#### ALIGNMENTS

1 MRCLPVFVILLLITASGPSVDAR--LKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58 "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.",
"Mechanisms for Bvol. 18:120-131(2001).
BMOL. Biol. Bvol. 18:120-131(2001).
EMBL; AP214980; AAG60408.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0019070; F:toxin activity; IEA.
GO; GO:0009406; P:toxin activity; IEA.
InterPro; IPR004214; Conocoxin.
Pfam; PF02950; Conotoxin; 1.
SEQUENCE 64 AA; 6928 MW; OABB7620FCCC1410 CRC64; 2; Gaps Bukaryota, Metazoa, Mollusca; Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus. SEQUENCE FROM N.A. MEDLINE=21105969; PubMed=11158371; Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., 83.4%; Score 276; DB 5; Length 64; 84.4%; Pred. No. 9.9e-29; iive 3; Mismatches 5; Indels 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 64 AA. PRT; Conotoxin scaffold IX.
Conus pennaceus (Feathered cone) . Similarity 84.4%; 54; Conservative PRELIMINARY; 59 FPCG 62 Fainzilber M.; Query Match Best Local S Matches 54 Q9BPE9 RESULT 1 Q9BPE9 셤 ò ð

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61 vPCG 64

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RESULT 2 Q9BPF1

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"Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF215098; AAG60519.1; -.
EMBL; AF214954; AAG60382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
"Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
MOL. Biol. Evol. 18:120-131(2001).
BMBL; AF215096; AAG60191.1; -.
BMBL; AF218096; AAG60191.1; -.
GO; GO:000576; C:extracellilar; IEA.
GO; GO:001570; F:toxin activity; IEA.
GO; GO:0015070; F:toxin activity; IEA.
InterPro; IPR004214; Conctoxin.
Fram; PP02950; Contoxin; L.
SEQUENCE 61 AA; 6697 MW; FBCAA26F92EE8900 CRC64;
1 MRCLPVFVILLLILIASAPSVDAQPKTKDDIPQASFLDNAKRYLQVLESKRNCCRRQIC--
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Neogastropoda; Conoidea; Conidae; Conus
                                                                                                                                                                                                                                                   Conotoxin scaffold IX precursor.

Conus textile (Cloth-of-gold come).

Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
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Pred. No. 7.1e-17;
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GO; GO:0015070; F:toxin activity; IEA
GO; GO:0009405; P:pathogenesis; IEA.
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                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conotoxin scaffold IX precursor. Conus pennaceus (Feathered cone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 56.2%;
Local Similarity 71.7%;
les 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7127 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AA;
                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6494;
                                                                             CG 60
                                           62
                                           61 CG
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                                                                                                                                                                                            Q9BH21;
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                                                                                                                                     RESULT 4
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EMBL; AF214959; AAG60387.1; -..

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0015070; F:toxin activity; IEA.

GO; GO:0015070; P:toxin activity; IEA.

InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214978; AAG60406.1; -.
GO; GO:0005576; C:extracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRCLPVFVILLLITASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC--GYKLC
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Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                               Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 192; DB 5; Length 63;
Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 196; DB 5; Length 64;
Pred. No. 3.6e-18;
3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAADCCFB2F12EF0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7374 MW; F7C8CD0192FC5C8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel, 17, Last sequence update) 01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AA.
                                                                                       64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0015070; F:toxin activity; IEA.
GO:0009405; P:pathogenesis; IEA.
erPro; IPR004214; Conotoxin.
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                                                                                                                           (TrEMBLrel. 17, Created) (TrEMBLrel. 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                 Conus pennaceus (Feathered cone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 58.0%;
1 Similarity 64.5%;
40; Conservative 6
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SEOUENCE 63 AA; 7091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.2%;
Best Local Similarity 68.3%;
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02950; Conotoxin;
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                                                                                           PRELIMINARY;
                                                                                                                                                                                  Conotoxin scaffold IX.
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Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 AA;
                                                                                                                             01-JUN-2001
01-JUN-2001
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                                                                                                                Q9BPF1;
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                                                                                         Q9BPF1
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RESULT 3

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O9BPG9

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Gaps

Length 61; 10; Indels

53 53 ö

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Gaps

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23 53

Q9BPF2

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Q9BPR2
AC Q9BP AC Q9BP DT 01-J
DT 01-

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"Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214969; AAG60397.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKL--C
                                                                                                    1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                                                                                                                      1 MRCFPVFIILLLAMASAPSFDARPKTEDDVPLSSFRDNLKRTLRTLLDDRRCC
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
                                        Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 182; DB 5; Length 62,
Pred. No. 2.4e-16;
3; Mismatches 16; Indels
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 9DF1B0FFAF2D8BAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AA; 6909 MW; 146E5C95794E6B70 CRC64;
                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                        13;
                                  Score 183; DB 5;
Pred. No. 1.8e-16;
3; Mismatches 13;
                                                                                                                                                                                                                              62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AA.
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GO; GO:0015070; F:toxin activity; IER
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conocoxin.
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                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                    Conus pennaceus (Feathered cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus pennaceus (Feathered cone).
                                  55.3%;
7163 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 65.6%;
40; Conservative
            55.0%;
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                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                  Conotoxin scaffold IX.
63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=37335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=37335;
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SEQUENCE
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Matches
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09BPG0
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EMBL; AF214977; AAG6405.1; ---
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:toxin activity; IEA.
InterPro; IPR004214; Conotoxin; IEA.

Pfam; PF02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).

EMBL, AF214931, AAGGA11.1; -.
GO, GO:0005576, C:extracellular; IEA.
GO; GO:00034057; F:toxin activity; IEA.
GO; GO:00094055, P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin;
                                             Gaps
                                                                                53
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0
                                                                       1 MRCLPVFVILLLITASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
                                                                                             Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC
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Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDINES 11158371;
MEDINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.;
       Score 186; DB 5; Length 62;
Pred. No. 7.2e-17;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 61;
                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AA; 6751 MW; 95754779BC12FE9B CRC64;
                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 183; DB 5;
Pred. No. 1.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
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                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                     Conus ventricosus (Mediterranean cone)
                                                                                                                                                                                                                                    Created)
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01-JUN-2001 (TrEMBLrel. 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus pennaceus (Feathered cone).
   56.2%;
ilarity 69.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.3%;
                                                                                                                                                                                                                                               (TrEMBLrel. 17, (TrEMBLrel. 25,
                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17,
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                     Conotoxin scaffold IX.
Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=117992;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conotoxin scaffold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=37335;
                                                                                                                                                                                                                                                                   01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                               Q9BPF2;
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Q9BPE7; Q9BPE7

RESULT 7

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1;

2; Gaps

28

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/ Match 53.6%;
Local Similarity 71.7%;
nes 38; Conservative 4
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NCBI_TaxID=101317;
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Matches
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Mol. Biol. Bvol. 18:120-131(2001).

EMBL; AF214960; AAG60388.1; -.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0015070; F:toxin activity; IEA.

GO; GO:0019405; P:pathogenesis; IEA.

InterPro; IPR004214; Conotoxin.

Pfam; PF02950; Conotoxin; 1.
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Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

Neogastropoda; Conoidea; Conidae; Conus.
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.4%; Score 180; DB 5; Length 62; llarity 59.7%; Pred. No. 4.5e-16; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                               Length 64;
                                                                                                                                                                                                                                                                                                                                                                                        19; Indels
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        GO; GO:0005576; C:extracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR04214; Conotoxin.
Fram; PP02950; Conotoxin. 1.
SEQUENCE 64 AA; 7146 MW; 5E5A04C6B6ADDF88 CRC64;
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Last sequence update)
Last annotation update)
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                      Score 181; DB 5;
Pred. No. 3.4e-16;
3; Mismatches 19;
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5%;
Matches 40; Conservative
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Best Local Similarity
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Q9BPG8
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"Mechanisms for 18:120-131(2001).

MOI. Biol. Evol. 18:120-131(2001).

EMBL; AF214972; AAG60400.1; -.

EMBL; AF214972; AAG60400.1; -.

GO; GO:000550; C:membrane, IEA.

GO; GO:00160233; F:peptidase activity; IEA.

GO; GO:00190019; F:pothogenesis; IEA.

GO; GO:0009405; P:proteolywis; and peptidolysis; IEA.

InterPro; IPR004214; Conotoxin.

InterPro; IPR0045060508; Peptidase_226.

Pfam. PR00560: Conotoxin.
                                                                                                                        "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
Mol. Biol. Bvol. 18:120-131(2001).
EMBL, AF214973, AAG6041.1;
GO: GO:0005576; C:extracellular; IEA.
GO: GO:0005405; P:toxin activity; IEA.
GO: GO:000406; P:pathogenesis; IEA.
Interpro; IPR004214; Conotoxin.
Fram, PP02950; Conotoxin, IBA.
SEQUENCE 59 AA; 6623 MM; BB61E25E8E1AB380 CRC64;
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
SEQUENCE FROM N.A. MEDLINE21105969; PubMed=11158371; Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Painzilber M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 177.5; DB 5; Length Pred. No. 9.1e-16; Mismatches 10; Indels
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PROSITE; PS00761; SPASE I 3; 1.
SEQUENCE 64 AA; 6982 MW; 85698912BA2104EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Conotoxin scaffold IX.
Conus ventricosus (Mediterranean cone).
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Best Local Similarity 65.6%; Pred. No. 1.2e-15;
Matches 42; Conservative 3; Mismatches 17;
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Best Local Similarity
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                      Matches
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Matches
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EMBL, AP214971; AAG60399.1; -..
GO; GO:0005576; Castracellular; IEA.
GO; GO:000570; F:toxin activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE S.G. Gilda Y., Avidan N., Ben-Asher E., Levy Z.,

Conticello S.G., Gilda Y., Avidan N., Ben-Asher E., Levy Z.,

Rainzilber M.;

"Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";

Mol. Biol. Evol. 18:120-131(2001).

EMBL; AF214956; AAG60384.1; -.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0015079; F:calcium ion binding; IEA.

GO; GO:0015070; F:toxin activity; IEA.

GO; GO:0016042; P:lipid catabolism; IEA.

GO; GO:0016045; P:plipid catabolism; IEA.

GO; GO:0009465; P:plipid catabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                     Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                      Score 174.5; DB 5; Length 63;
Pred. No. 2.4e-15;
7; Mismatches 17; Indels
                                                                                                                                                               MEDIINE=21105569; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Mollúsca; Gastropoda; Orthogastropoda;
                                                                                                                                                                                                                                                                                                              6878 MW; 27DD9A64D056B548 CRC64;
                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6563 MW; D8B7537B6B516BBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
     63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AA
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InterPro; IPR001211; PhospholipaseA2.
  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus textile (Cloth-of-gold cone).
                                                                         Conus pennaceus (Feathered cone)
                                                                                                                                                                                                                                                                                                                                      52.7%;
60.3%;
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PROSITE; PS00118; PA2 HIS; 1
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                                                                                                                                                                                                                                                                                                                                                              38; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                               Conotoxin scaffold IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conotoxin scaffold IX.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                              63 AA;
                                                                                                                           NCBI_TaxID=37335;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AA;
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Matches
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Score 173; DB 5; Length 58;

52.3%;

Query Match

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                                                                               1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLORHQDK--SVCCGYKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF214975; AAG60403.1; -
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:001405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRCLPVFVILLLLTASGPSVDARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCC-GYKLCF
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan'N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 63;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.5%; Score 170.5; DB 5; Length 55.6%; Pred. No. 8.2e-15; 1.1 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77ED864BFD7FAE50 CRC64;
                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
  Pred. No. 3.5e-15;
3; Mismatches 12;
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                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seg
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                   Conus pennaceus (Feathered cone).
(80.59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6993 MM;
                      Conservative
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 55.6
tes 35; Conservative
                                                                                                                                                                                                                                                                                                Conotoxin scaffold IX
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=37335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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                        39;
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

Run on:

August 10, 2004, 15:55:40 ; Search time 15.5676 Seconds (without alignments) 217.797 Million cell updates/sec

US-10-072-602B-534 Perfect score:

1 SVCCGYKLCFPC 12 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\*
1: geneseqpl9\*\*
2: com geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s.\* geneseqp1990s.\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2000s:\* geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STRAMMERS

IES	Description	1	Collus	Conus	conus		AGDOODE AMINO ACT	Aays222 CHI-COHOI	CIII - C	٠,	Chi-co	Amino		Abg99748 Conus sp	Abg99739 Conus sp	Conus	Conus			Control	Compa	ייייייייייייייייייייייייייייייייייייייי	Abg99602 Conus sp	Conus	פוועט	Control	Abassan Collus sp	conne	ADGRADE COURS SP
SUMMARIES	ID	ABG99749	ABG99600	ABG99744	ARGOGERA	AAROROTR	AAY92229	AAY92230	AAB08017	AAY92231	AABOROTE	ARG99595	000000	ABG99748	ABGYY 13 Y	ABG99743	ABG99742	ABG99741	ABG99753	ABG99740	ABG99750	ABG00502	7000000	ABG99400	ABG99598	ABG99591	ABG99470	ABG99587	
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•∤•	Query Match	100.0	100.0	87.3	87,3	86.1	86.1	86.1	86.1	86.1	86.1	9	797	10.		י ע	o.	ė.	79.7	79.7	79.7	79.7	o	n o	٠	79.7	79.7	79.7	
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63 79.7 64	79.7	78.5	78.5	74.7	74.7		74.7	74.7	74.7	73.4	73.4	* (	0.60	69.6	68.4	68.4	54 68.4 12	54 68.4 13	4		54 68.4 13
26	17	87	53	30	31	32	33	34	35	36	3.7		0 0	بر ا	40	41	42	43	44	3.6	n <b>!</b>

#### ALIGNMENTS

ABG99749 standard; peptide; 12 AA. RESULT 1 ABG99749

(first entry) 17-JAN-2003

ABG99749;

Conus sp conotoxin-associated peptide SEQ ID 534.

Conotoxin; come snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.

Conus aulicus.

WO200264740-A2.

22-AUG-2002.

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.

Ξ.Ξ. Garrett JE, Cruz Watkins M, Garret letty R, Jones RM, BM, Mcintosh JM, Watkins M, Walker CS, Shetty R, Olivera | Grilley |

WPI; 2002-706921/76.

New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

Claim 1; Page 287; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders. The radiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for 

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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analyesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders. The radiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for characterising an ew site on these receptors or channels, and for screening and identifying novel small molecules that interact with the screening and identifying novel small molecules that interact with the schove-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
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screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
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Μ;
                                                                                                                            Length 12;
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etty R, Jones RM, Schoenfeld
                                                                                                                Score 79; DB 5; Length LA. Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                                                                                                                                        Comus sp conotoxin-associated protein SEQ ID 352.
                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 1; Page 239; 305pp; English
                                                                                                                                                                                                                                                                                                                        ABG99600 standard; protein; 62 AA.
                                                                                                                                100.0%;
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UNIV UTAH RES FOUND.
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Walker CS, Sl
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                                                                                                                                                                  Conservative
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N-PSDB; ABX04937.
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nes 12; Conserv
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                                                                                                 Sequence 12 AA
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Grilley M,
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                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                          Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
ligand-gated ion channel modulator; pain-relief.
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Jones RM, Schoenfeld RM;
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              Indels
                                                                                                                                                                                                                                              Conus sp conotoxin-associated peptide SEQ ID 529.
Pred. No. 0.0009; Mismatches 0;
                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 287; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shetty R,
                                                                                                                                                         ABG99744 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                    17-JAN-2003 (first entry)
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Walker CS, S
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                                                                     50 SVCCGYKLCFPC
                                                1 SVCCGYKLCFPC
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                Conus marmoreus
                                                                                                                                                                                                                                                                                                                                                            WO200264740-A2.
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Grilley M,
                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2002.
                                                                                                                                                                                                                                                                                     Conotoxin;
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Best Local &
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DB 5; Length 62;

100.0%; Score 79;

Sequence 62 AA;

Query Match

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AAY92229
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                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated in channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for channel disorders, ligand-gated ion these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                          New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.
                                                                                              Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
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                                                                                                                                                                                                                                                                          Ξ.Ξ.
                                                                                                                                                                                                                                                                      Watkins M, Garrett JE, Cruz
etty R, Jones RM, Schoenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                           Conus sp conotoxin-associated protein SEQ ID 330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of the conotoxin peptide Mar2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69; DB 5
Pred. No. 0.021
0; Mismatches
            ABG99585 standard; protein; 61 AA
                                                                                                                                                                                                                                                                                Shetty R,
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 231; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB08018 standard; peptide; 12 AA.
                                                                                                                                                                                            11-FEB-2002; 2002WO-US003887.
                                                                                                                                                                                                                09-FEB-2001; 2001US-0267408P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.3%;
                                                                                                                                                                                                                                    (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                      (first entry)
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                                                                                                                                                                                                                                                                              Walker CS,
                                                                                                                                                                                                                                                                                                WPI; 2002-706921/76.
N-PSDB; ABX04930.
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nes 10; Conser
                                                                                                                             Conus marmoreus
                                                                                                                                                 WO200264740-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 61 AA;
                                                    17-JAN-2003
                                                                                                                                                                                                                                                                    Olivera BM,
Grilley M,
                                                                                                                                                                       22-AUG-2002
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                                 ABG99585
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Best Loc
Matches
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The present sequence represents an ap-conotoxin peptide, designated Marz. Conotoxins are naturally available in minute amounts in the venom of cone snails. The peptides have analgesic activity. The peptides are used to treat or prevent pain. note: this sequence does not appear in the specification; it was created using information provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chi-conotoxin; chi-MrIA; cone snail; inhibitor; amine transporter;
neuronal; noradrenaline transporter; urinary tract disorder; analgesic;
antiarrhythmic; cardiant; antidepressant; anxiolytic; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Ap-conotoxin; conotoxin; venom; cone snail; analgesic; pain; Mar2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purified ap-conotoxin derived from cone snail venom for use as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 3; Length 12;
Pred. No. 0.0072;
0; Mismatches 1; Indels
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/note= "4-hydroxyproline"
                                                                                                                                /note= "hydroxy-Pro"
                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                     Cruz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chi-conotoxin peptide, chi-MrIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page; 29pp; English.
                                                                                                                                                                                                                                                              2000WO-US001978.
                                                                                                                                                                                                                                                                                                         99US-0118381P.
99US-0173343P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.1%;
90.9%;
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Best Local Similarity 90.5
Matches 10; Conservative
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                                             Conus marmoreus
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                                                                                                                                                                      WO200044769-A1
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                                                                                     Key
Modified-site
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                                                                                                                                                                                                                                                            28-JAN-2000;
                                                                                                                                                                                                                                                                                                      29-JAN-1999;
28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mcintosh JM,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                           This conotoxin, chi-MrIA, is a member of a new class of conotoxins, designated chi-conotoxin. It was isolated from the venom of the mollusc bunting cone snail, Conus marmoreus. The peptide is an inhibitor of the mount and a mine transporters, especially the neuronal noradrenaline transporter. Inhibitors of noradrenaline re-upcake which have a negligible anti-cholinergic effect are particularly useful in the treatment of lower urinary tract disorders. Chi-MrIA (0.1 nM-1 micro M) inhibited the accumulation of radiolabeled noradrenaline in a concentration-dependent manner, with a log IC-50 value of -8.17 plus or minus 0.0275 (n = 4). The concentration of chi-MrIA required to inhibit concentration is approximately mass found to be approximately 7 nM. This concentration is approximately eneoter of magnitude lower than that needed for desipramine to produce the same effect. The peptides are useful for the treatment or prophylaxis of urinary or caradiovascular contraction is a phonomer of the urinary or caradiovascular contraction is a concentration is a concentration is a concentration or prophylaxis of urinary or caradiovascular contraction is a contraction is a concentration or prophylaxis of urinary or caradiovascular contraction can be contracted to the propertical contraction is a contraction or prophylaxis of urinary or caradiovascular contractions and contraction can be contracted to the contraction can be contracted to contract for contraction can be contracted to contract for candiovascular contractions can be contracted to contract for contraction 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conditions or diseases (arrhythmia or coronary heart failure) or mood disorders (depression, anxiety or cravings), or the treatment or control of pain or inflammation (chronic pain, neuropathic pain or inflammatory pain)
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                                                                                                                                        Isolated, synthetic or recombinant chi-conotoxin peptide capable of inhibiting neuronal amine transporter used for treatment or prophylaxis of urinary or cardiovascular conditions, mood disorders, or treatment/control of pain/inflammation.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.1%; Score 68;
90.9%; Pred. No.
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                                                                          Sharpe IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chi-conotoxin peptide, chi-MrIB.
                                                                                                                                                                                                                                   Claim 3; Page 33; 47pp; English.
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       98AU-00006274.
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                                        (UYQU ) UNIV QUEENSLAND
                                                                          Alewood PF,
                                                                                                           WPI; 2000-303738/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
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       02-OCT-1998;
                                                                          Lewis RJ,
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This conotoxin, chi-MrIB, is a member of a new class of conotoxins, designated chi-conotoxin. It was isolated from the venom of the mollusc bunting cone snall, Conus marmoreus. The peptide is an inhibitor of the mouronal amine transporters, especially the neuronal noradrenaline reneuronal amine transporters, especially the neuronal noradrenaline transporter. Inhibitors of noradrenaline re-uptake which have a reatment of lower urinary tract disorders. Chi-MrIA (0.1 nM-1 micro M) inhibited the accumulation of radiolabeled noradrenaline in a inhibited the accumulation of radiolabeled noradrenaline in a innus 0.0275 (n = 4). The concentration of chi-MrIA required to inhibit the accumulation by 50 percent was found to be approximately 7 nM. This concentration is approximately one order of magnitude lower than that concentration is approximately one order of magnitude lower than that useful for the treatment or prophylaxis of urinary or cardiovascular useful for the treatment or prophylaxis of urinary or cardiovascular conditions or diseases (arrhythmia or coronary hear failure) or mood
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                                                                                                                                                                                                                         inhibiting neuronal amine transporter used for treatment or prophylaxis of urinary or cardiovascular conditions, mood disorders, or treatment/control of pain/inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders (depression, anxiety or cravings), or the treatment or contro
of pain or inflammation (chronic pain, neuropathic pain or inflammatory
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                                                                                                                                                                                             synthetic or recombinant chi-conotoxin peptide capable of
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                                                                   Sharpe IA;
                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 33; 47pp; English.
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(UYQU ) UNIV QUEENSLAND.
                                                                       Lewis RJ, Alewood PF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCCGYKLCHPC
                                                                                                                                       WPI; 2000-303738/26.
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Best Local Similarity
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Gaps

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Length 61; 1; Indels

86.1%; Score 68; DB 3; 90.9%; Pred. No. 0.028; live 0; Mismatches I

10; Conservative 2 VCCGYKLCFPC 12

61

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minus 0.0275 (n = 4). The concentration of chi-MrIA required to inhibit the accumulation by 50 percent was found to be approximately 7 nm. This concentration is approximately one order of magnitude lower than that needed for desipramine to produce the same effect. The peptides are useful for the treatment or prophylaxis of urinary or cardiovascular conditions or diseases (arrhythmia or coronary heart failure) or mood disorders (depression, anxiety or cravings), or the treatment or control of pain or inflammation (chronic pain, neuropathic pain or inflammatory)
                                                                                                                                                                                                                                                                                                                                                                                                                                         51 VCCGYKLCHPC
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   Sequence 61 AA;
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                                                                                                                                                                                                                                                   of cone
                                                                                                                                                                                                         The present sequence represents an ap-conotoxin peptide, designated Marl. Conotoxins are naturally available in minute amounts in the venom of cone snails. The peptides have analgesic activity. The peptides are used to treat or prevent pain. note: this sequence does not appear in the specification; it was created using information provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chi-conotoxin; chi-MrIA; cone snail; inhibitor; amine transporter;
neuronal; noradrenaline transporter; urinary tract; analgesic; cardiant;
antiarrhythmic; antidepressant; anxiolytic; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the conotoxin, chi-MrIA, a member of a new class of conotoxins, designated chi-conotoxin. It was isolated from the venom of the mollusc hunting cone snail, Conus marmoreus. The peptide is an inhibitor of the neuronal amine transporters, especially the neuronal noradrenaline transporter. Inhibitors of noradrenaline re-uptake which have a negligible anti-cholinergic effect are particularly useful in the treatment of lower urinary tract disorders. Chi-MrIA (0.1 nM-1 micro M) inhibited the accumulation of radiolabeled noradrenaline in a concentration-dependent manner, with a log IC-50 value of -8.17 plus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated, synthetic or recombinant chi-conotoxin peptide capable of inhibiting neuronal amine transporter used for treatment or prophylaxis of urinary or cardiovascular conditions, mood disorders, or treatment/control of pain/inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                         Purified ap-conotoxin derived from cone snail venom for use as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chi-conotoxin, chi-MrIA, leader and mature peptide.
                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 3;
Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY92231 standard; protein; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 31; 47pp; English.
       Cruz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharpe
                                                                                                                                                             Claim 13; Page; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                86.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-AU000844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98AU-00006274
    Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VCCGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYQU ) UNIV QUEENSLAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCCGYKLCHPC
                                                WPI; 2000-476222/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-303738/26.
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                                                                                                                                                                                                                                                                                                                                                      Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus marmoreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200020444-A1
  Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-APR-2000.
                                                                                                                       analgesic.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY92231;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
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LD AAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a Marl propeptide. Marl is an apconotoxin peptide. Conotoxins are naturally available in minute amount venow of cone snails. The peptides have analgesic activity. peptides are used to treat or prevent pain
                                                                                                                                            Ap-conotoxin; conotoxin; venom; cone snail; analgesic; pain; Marl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purified ap-conotoxin derived from cone snail venom for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68; DB 3; Length 61;
Pred. No. 0.028;
0; Mismatches 1; Indels
                                                                                                          Amino acid sequence of the conotoxin Marl propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Page 13-14; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Cruz LJ;
AAB08016 standard; protein; 61 AA.
                                                                                                                                                                                                                                                                                               28-JAN-2000; 2000WO-US001978.
                                                                                                                                                                                                                                                                                                                                 99US-0118381P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                     (UTAH ) UNIV UTAH RES FOUND.
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 VCCGYKLCHPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-476222/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                    Conus marmoreus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA63513
                                                                                                                                                                                                                         WO200044769-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                 29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                   28-DEC-1999;
                                                                        14-NOV-2000
                                                                                                                                                                                                                                                             03-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analgesic.
                                      AAB08016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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RESULT 11

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ABG99595

ABG99595

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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptors or receptor characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99386-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
ligand-gated ion channel modulator; pain-relief.
        Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
ligand-gated ion channel modulator; pain-relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.7%; Score 63; DB 5; Length 11; 90.0%; Pred. No. 0.032; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                 Watkins M, Garrett JE, Cruz
etty R, Jones RM, Schoenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus sp conotoxin-associated peptide SEQ ID 524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG99739 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                         Shetty R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 287; 305pp; English.
                                                                                                                                                                                                        11-FEB-2002; 2002WO-US003887.
                                                                                                                                                                                                                                               09-FEB-2001; 2001US-0267408P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.06;
                                                                                                                                                                                                                                                                                      (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
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Best Local Similarity 90..
Best 2 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                     Mcintosh C
Walker CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGYKLCSPC
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-706921/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      channel disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus bandanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200264740-A2
                                                                              Conus bandanus.
                                                                                                                       WO200264740-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                     Olivera BM,
Grilley M,
                                                                                                                                                                 22-AUG-2002
                   Conotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters.

ABG99360-ABG99853 represent the conotoxin protein and peptides described
                                                                                                                                                                                    Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about be subjected to a pain-causing event, or for treating voltage-gated io
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0
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Jones RM, Schoenfeld RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus sp conotoxin-associated peptide SEQ ID 533.
                                                                                                                                                 Conus sp conotoxin-associated protein SEQ ID 345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.028;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG99748 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 236; 305pp; English.
                            ABG99595 standard; protein; 61 AA.
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2002; 2002WO-US003887.
                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2001; 2001US-0267408P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
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                                                                                                            (first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walker CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 VCCGYKLCHPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-706921/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABX04935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 61 AA;
                                                                                                                                                                                                                                                              Conus marmoreus
                                                                                                                                                                                                                                                                                                   WO200264740-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olivera BM,
                                                                                                               17-JAN-2003
                                                                                                                                                                                                                                                                                                                                             22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grilley M,
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Gaps

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RESULT 12 ABG99748

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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders. Ilgand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described
                                                                                                                                                                                                            New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
                                                                                                                                    Watkins M, Garrett JE, Cruz
etty R, Jones RM, Schoenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.7%; Score 63; DB 5; Length 11; 90.0%; Pred. No. 0.032; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcintosh JM, Watkins M, Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus sp conotoxin-associated peptide SEQ ID 528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the disclosure of the invention
                                                                                                                                                 Shetty R,
                                                                                                                                                                                                                                                                                            Claim 1; Page 286; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG99743 standard; peptide; 12 AA.
                  11-FEB-2002; 2002WO-US003887.
                                                 09-FEB-2001; 2001US-0267408P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-2002; 2002WO-US003887.
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                                                                               (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND
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(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                  Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CCGYKLCSPC 11
                                                                                                                                                 Walker CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CCGYKLCFPC 12
                                                                                                                                                                              WPI; 2002-706921/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                Olivera BM,
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                                                                                                                                                Grilley
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Cruz LJ;

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alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.
                                                                                                                                                                                     genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conocoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be
                                                                                                                                                                                                                                                  subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders. ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99851 represent the conotoxin protein and peptides described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.
                                                                                                                                                                      This invention describes novel conotoxin peptides from the cone snail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                  pain reliever for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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    Schoenfeld RM;
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netty R, Jones RM, Schoenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus sp conotoxin-associated peptide SEQ ID 527.
                                                              peptides, useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 5;
Pred. No. 0.035;
   Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
 Shetty R,
                                                                                                                                         Claim 1; Page 286; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG99742 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             79.7%;
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(UTAH ) UNIV UTAH RES FOUND.
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                                                             New cone snail conotoxin
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Walker CS, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVCCGYKLCFPC 12
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 Walker CS,
                               WPI; 2002-706921/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-706921/76.
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Best Local Similarity
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Grilley M,
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Grilley M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conotoxin;
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This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated in channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated in channel disorders. The radiolabeled conotoxin peptide is also useful characterising a new site on these receptors or characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the absorpance channels or receptors, which are monoamine transporters. ABG09386-ABG39883 represent the conotoxin protein and peptides described in the disclosure of the invention
Claim 1; Page 286; 305pp; English.
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Sequence 12 AA;

0; Gaps Score 63; DB 5; Length 12; Pred. No. 0.035; 2; Mismatches 2; Indels Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative

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1 SVCCGYKLCFPC 12 | |||:|:| || 1 STCCGFKMCIPC 12

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Search completed: August 10, 2004, 16:02:37 Job time: 15.5676 secs

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RESULT 2
US-09-336-536-60
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Sequence 60,
Sequence 13,
Sequence 29,
Sequence 29,
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-316-536-60
US-09-316-556-53
US-09-914-259-13
US-08-4877-383-29
US-08-4877-383-29
US-08-487-174-59
US-08-480-750-29
US-08-480-750-59
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US-08-480-750-44
US-08-480-750-35
US-08-487-174-35
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US-08-487-174-25
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 55, Application US/09336536; Patent No. 6406884; GENERAL INFORMATION:
; APPLICANT: Leiby, K.; APPLICANT: Bossone, S.; APPLICANT: Bossone, S.; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF; CURRENT APPLICANION NUMBER: US/09/336,536; CURRENT FILING DATE: 1999-06-18; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 65; LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOCATION:
APPLICANT: MCKAY, C.
APPLICANT: BOSONG, S.
TITLE OF INVENTIONS SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT FAPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 60
LENGTH: 187
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US-08-487-174-57
US-08-480-750-57
US-08-480-750-57
US-08-487-174-56
US-08-137-800-40
US-08-137-800-40
US-08-137-800-40
US-08-137-800-42
US-08-487-174-42
US-08-477-383-42
US-08-477-383-42
US-08-137-800-41
US-08-137-800-41
US-08-137-800-41
US-08-137-800-41
US-08-137-800-41
US-08-137-800-41
US-08-137-800-41
US-08-137-800-41
US-08-137-800-41
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Best Local Similarity 63.0
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CORGANISM: Mus musculus
US-09-336-536-65
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COMPUTER READABLE FORM:
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ZIP: 20005
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US-08-477-383-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                     Indels
                                                                                                                                                                                                                     APPLICANT: LICORALIAN:
APPLICANT: MCKAY, C.
APPLICANT: MCKAY, C.
APPLICANT: MCKAY, C.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARES PATENTIN Ver. 2.0
SEQ ID NO 58
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hyman, Paul
APPLICANT: Williams, Wark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REPERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT PILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 503
                     3;
   Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                         Sequence 58, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
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Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/08137800 Patent No. 5514774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT CORGANISM: Drosophila melanogaster US-09-914-259-13
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                    106 SCCCLYKMCCP 116
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                                                     1 SVCCGYKLCFP 11
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; ORGANISM: Mus musculus
US-09-336-536-58
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hes 5; Conserv
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APPLICANT: Olivers
                                                                                                                                                        US-09-336-536-58
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US-09-914-259-13
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
APPLICANT: Hillyard, David R.
APPLICANT: McIncosh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ventable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Xaa is des-Xaa or
Gly-Arg-Arg-Asn-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                          CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFRONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24260-104763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/08477383;
Patent No. 5589340;
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M. APPLICANT: Cruz, Lourdes J. APPLICANT: Hillyard, David R. APPLICANT: Macintosh, J. Michael APPLICANT: Santos, Ameurfino S. TITLE OF INVENTION: Conotoxin Peptic NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Conus stercusmuscarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVCCGY---KLCFPC 12
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10 TTCCGYDPGSMCPPC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 37..38
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                            STREET: 1201 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1201 New CITY: Washington STATE: DC
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LOCATION: 38
OTHER INFORMATION: /note= "Xaa is des-Xaa or
OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
OTHER INFORMATION: preferably amidated."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                           24260-107673
       APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-UNN-1995
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-UUN-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIPICATION: 530
PILOR APPLICATION DATE: US 08/137,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus stercusmuscarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/08480750
Patent No. 5633347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                          NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24;
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
TELEPAX: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVCCGY---KLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |||| : |||
10 TTCCGYDPGSMCPPC 24
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Best Local Similarity 46.74
Conservative
7:
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 38 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DC COUNTRY: U
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-480-750-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-487-174-29
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OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
OTHER INFORMATION: preferably amidated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.1%; Score 43.5; DB 1; Length 38; Best Local Similarity 46.7%; Pred. No. 8.7; Matches 7; Conservative 2; Mismatches 3; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/137,800
FILING APPLICATION NUMBER: US 08/137,800
FILING APPLICATION NUMBER: US 08/137,800
FILING APPLICATION NUMBER: US 08/084,848
FILING APPLICATION NUMBER: US 08/084,848
FILING APPLICATION NUMBER: 28.957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELEFRANION NUMBER: 28,957
TELEFRANION NUMBER: 28,957
TELEFRANION NUMBER: 20.962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baetjer, Howard & Civiletti
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
SIRFFT: STRFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/08487174

Patent No. 5595972

GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Hallyard, David R.
APPLICANT: Santos, Ameurfino S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Conus stercusmuscarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVCCGY---KLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 TTCCGYDPGSMCPPC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-487-174-29
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCETARING SILEM:
SCETARING SILEM:
SCETARING SILEM:
SCETARING APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
OLGASSIFICATION 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
SILING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER:
SILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
ANNUMBER APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
ANNUMBER APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
ANNUMBER APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.1%; Score 43.5; DB 1; Best Local Similarity 46.7%; Pred. No. 9.4; Matches 7; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-487-174-59
Sequence 59, Application US/08487174
Sequence 59, Application US/08487174
Patent No. 5595972
APPLICANT: Olivera, Baldomero M. APPLICANT: CTuz, Lourdes J. APPLICANT: Hillyard, David R. APPLICANT: Macintosh, J. Michael APPLICANT: Santos, Ameurfino S. TITLE OF INVENTION: Conctoxin Peptides NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADRESS:
                                                     24260-107673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Conus stercusmuscarum
US-08-477-383-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
RAME: Ihnen, Jeffrey L.
REGISTATION UNDRER: 28,957
REFERENCE/DOCKET NUMBER: 2426(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-8300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE GHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVCCGY---KLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TTCCGYDPGSMCPPC 24
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LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                           TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "Xaa is des-Xaa or cother InFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is CHER INFORMATION: preferably amidated." When Xaa is des-Xaa the C-terminus is US-08-480-750-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.1%; Score 43.5; DB 1; Length 38; 46.7%; Pred. No. 8.7; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Macintos J.
APPLICANT: Macintos, Ameurfino S.
TITLE OF INVENTION: Conctoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                              REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-8300
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acids
STRANDEDNESS:
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-4UN-1993
ATORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus stercusmuscarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 59, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVCCGY---KLCFPC 12
FILING DATE: 19-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 TTCCGYDPGSMCPPC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site LOCATION: 38
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus stercu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 46.7 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Matches
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1 SVCCGY---KLCFPC 12

à

linear

TOPOLOGY:

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55.1%; Score 43.5; DB 1; Length 80; 46.7%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                 B: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue N.W., Suite 1000
                                                                                                         APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: McIntola Bapticant: McIntola Bapticant: Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS: ADDRESSE: Venable, Bar.
CITY: War.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Sancos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24260-104763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus stercusmuscarum
                                                                                                  US-08-137-800-44; Sequence 44, Application US/08137800 Patent No. 5514774; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISCRATION NUMBER: 28,957
REPRENCE/DOCKET NUMBER: 2426
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVCCGY---KLCFPC 12
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             10 TTCCGYDPGSMCPPC 24
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SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20002
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US-08-477-383-44
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                                                                                                                         Query Match 55.1%; Score 43.5; DB 1; Length 42; Best Local Similarity 46.7%; Pred. No. 9.4; Matches 7; Conservative 2; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DAMER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTOMENEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.1%; Score 43.5; DB 1; Best Local Similarity 46.7%; Pred. No. 9.4; Matches 7; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintcosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conctoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDECE ADDRESS:
CORRESPONDECE ADDRESS:
STREET: 1201 New York Avenue, N.W., Sui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24260-107673
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                                                                  ORGANISM: Conus stercusmuscarum
                                                                                                                                                                                                                                                                                                                                                                   Sequence 59, Application US/08480750; Patent No. 5633347; GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                     1 SVCCGY---KLCFPC 12
                                                                                                                                                                                                                                              : | | | | : | | | | 10 TTCCGYDPGSMCPPC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
                    HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
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                                                                                    US-08-487-174-59
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Length 80;
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APPLICATION NUMBER: US/08/480,750 FILING DATE: 0.7-UM-1995 CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800 FILING DATE: 19-OCT-1993 PRIOR APPLICATION NUMBER: US 08/184,848 FILING DATE: 29-UM-1993 ATPLICATION NUMBER: US 08/084,848 FILING DATE: 29-UM-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43.5; I
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44, Application US/08480750
Patent No. 553347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
ITITE OF INVENTION: Conotoxin Peptides
INWHER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    24260-107673
                    APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-UN-1995
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/084,848
FILING DATE: 29-UN-1993
ATTORNEY/AGENT INPORMATION:
REGISTATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-10767;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-962-8300
INFORMATION FOR SEQ. 1D NO: 44:
LEMOCTH: OR AMENICATICS: LEMOCTH: CONTACT RESIDENCE CHARACTER LESTICS:
LEMOCTH: OR AMENICATICS: LEMOCTH: CONTACT RESIDENCE CHARACTER LESTICS:
LEMOCTH: OR AMENICATICS: LEMOCTH: CONTACT RESIDENCE CHARACTER LESTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 TTCCGYDPGSMCPPC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVCCGY---KLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 80 amino acids
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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US-08-487-174-44

is Sequence 44, Application US/08487174

j Patent No. 555972

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.

ITILE OF INVENTION: Conotoxin Peptides

CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000

CITY: Washington

STATE: STATE: COUNTRY. T.
                                                                                                                        ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conus stercusmuscarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVCCGY---KLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.7'
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                              COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: COT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 20005
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Gaps

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Search completed: August 10, 2004, 16:05:36 Job time : 4.7027 secs

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349, App 162, App 342, App 364, App 364, App 552, App 5532, App 523, App 223, App 351, App 361, App 36

Sequence Sequence Sequence

US-10-072-602B-349
US-10-072-602B-339
US-10-072-602B-162
US-10-072-602B-163
US-10-072-602B-364
US-10-072-602B-364
US-10-072-602B-532
US-10-072-602B-532
US-10-072-602B-532
US-10-072-602B-532
US-10-072-602B-531
US-10-072-602B-531
US-10-072-602B-537
US-10-072-602B-537
US-10-072-602B-537
US-10-072-602B-537
US-10-072-602B-163
US-10-072-602B-163
US-10-072-602B-163
US-10-072-602B-364
US-10-072-602B-334
US-10-072-602B-334
US-10-072-602B-334
US-10-072-602B-334
US-10-072-602B-334
US-10-072-602B-334
US-10-072-602B-334
US-10-072-602B-334
US-10-072-602B-334

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence 3 Sequence 3 Sequence 5

Sequence

Sequence 3 Sequence 3 Sequence 3 56089, A 362, App

Sequence

Sequence

US-10-072-602B-346 US-10-424-599-161903 US-10-425-114-56089 US-10-072-602B-362

ALIGNMENTS

Sequence Sequence

Sequence

Sequence

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Sequence
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                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/BCT NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-072-602B-352

US-10-072-602B-332

US-10-072-602B-345

US-10-072-602B-524

US-10-072-602B-524

US-10-072-602B-524

US-10-072-602B-528

US-10-072-602B-528

US-10-072-602B-528

US-10-072-602B-528

US-10-072-602B-538

US-10-072-602B-536

US-10-072-602B-536

US-10-072-602B-536

US-10-072-602B-536

US-10-072-602B-538

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                                                                                                                                                                                                              1291235 segs, 313682936 residues
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                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         using sw model
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Gapop 10.0 , Gapext 0.5
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79
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Maximum DB seq length: 2000000000
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Match Length
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86.11
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                                                         ì
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                                                                                                                                                       Sequence:
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                                                                                                                              Title:
Perfect
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RESULT 1

US-10-072-602B-534

i Sequence 534, Application US/10072602B

i Sequence 534, Application No. US20030109670A1

i GENERAL INFORMATION:
    APPLICANT: University of Utah Research Foundation
    APPLICANT: Olivers, Baldomero M.
    APPLICANT: Olivers, Baldomero M.
    APPLICANT: Gratett, James E.
    APPLICANT: Gratett, James E.
    APPLICANT: Gratett, James E.
    APPLICANT: Gratett, James E.
    APPLICANT: Gratett, Reshma
    APPLICANT: Grates E.
    APPLICA
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1 SVCCGYKLCFPC 12 ||||||||||||| 1 SVCCGYKLCFPC 12

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Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J, Michael
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Shefty, Reshma
APPLICANT: Shefty, Reshma
APPLICANT: Shefty, Reshma
APPLICANT: Ones, Robert M.
                                                                              Sequence 352, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIncsh, J, Michael
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                            APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Shetry, Reshma
APPLICANT: Shetry, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/072,602B CURRENT FILING DATE: 2002-02-11 PRIOR APPLICATION UNDRER: US 60/267,408 PRIOR FILING DATE: 2001-02-09 NUMBER OF SEQ ID NOS: 638 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 529, Application US/10072602B
Publication No. US20030109670A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 352
LENGTH: 62
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Matches 12, Conservative
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                                    RESULT 2
US-10-072-602B-352
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LENGTH: 13
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Score 69; DB 14; Length 13;
Pred. No. 0.007;
0; Mismatches 1; Indels
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Pred. No. 0.026;
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% Sequence 345, Application US/10072602B

% Publication No. US20030109670A1

% GENERAL INFORMATION:

% APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                           ; Sequence 330, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Cone Snail Peptides
TITLE OF INVENTION: Cone Snail Peptides
FILE REPERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR PEDING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
TITLE OF INVENTION: Cone Snail Peptides
FILE REPERBERS: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
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                                                                                                                                                                                                                                                                                                            Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert M.
Walker, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cognetix, Inc.
Clivera, Baldomero M.
McIntosh, J, Michael
Watkins, Maren
Garrett, James E.
Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert M.
  87.3%;
90.9%;
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus marmoreus
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                                                                                 2 VCCGYKLCFPC 12
                                                                                                                        3 VCCGYKLCLPC 13
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Gaps
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Pred. No. 0.039;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J, Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 528, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION;
; APPLICANT: University of Utah Research Foundation;
; APPLICANT: Cognetix, Inc.
; APPLICANT: Clivera, Baldomero M.
; APPLICANT: Matchosh, J. Michael
; APPLICANT: Matkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SEQ ID NO 527
LENGTH: 12
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR PILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 533
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cruzz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Robert M.
APPLICANT: Crois Shelley Robert M.
APPLICANT: Shetty, Robert M.
APPLICANT: Shetty, Robert M.
FILE REFERENCE: 2314-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 527, Application US/10072602B Publication No. US20030109670A1
                                                                                                                                                                                                                                                                                       79.78;
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66.7%;
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Best Local Similarity 66.7
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Best Local Similarity 90.0
Matches 9; Conservative
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ORGANISM: Conus pennaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 STCCGFKMCIPC 12
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                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Conus bandanus
US-10-072-602B-533
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APPLICANT:
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Pred. No. 0.036;
0; Mismatches 1; Indels
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; Sequence 533, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Wentuch, J, Michael
; APPLICANT: Warkins, Maren
; APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Utah Research Foundation APPLICANT: Coquetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Morinced. J, Michael
APPLICANT: Mathins, Maren
APPLICANT: Mathins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Michelle
APPLICANT: Grilley, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE REPERENCE: 2314-249
CURRENT APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2002-02-01
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert M.
Walker, Craig
Shetty, Reshma
    SOFTWARE: PatentIn version 3.0
SEQ ID NO 345
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.78;
                                                                                                                                            Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                 ; ORGANISM: Conus marmoreus
US-10-072-602B-345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Conus bandanus
US-10-072-602B-524
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Best Local Similarity
Matches 9; Conserv
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                                                                  TYPE: PRT
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University of Utah Research Foundation
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TITLE OF INVENTION. Cone Snail Peptides
FILE REPERBUCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                Cruz, Lourdes J.
Grilley, Michelle
Schoenfeld, Robert M.
Walker, Craig
Shetty, Reshma
                                                                          Olivera, Baldomero M.
McIntosh, J, Michael
Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 526
LENGTH: 13
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     US20030109670A1
                                                                                                                                 Garrett, James E.
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Best Local Similarity
Matches 8; Conserv
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APPLICANT:
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Pred. No. 0.045;
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                            APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US 60/267,408
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PATENTIN PATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 525, Application US/10072602B
Publication No. US20030109670A1
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US-10-072-602B-526
; Sequence 526, Application US/10072602B
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Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Cruz, Lourdes J.
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Schoenfeld, Robert M.
Walker, Craig
Shetty, Reshma
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SOFTWARE: Patentin version 3.0
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Garrett, James E.
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                   Cruz, Lourdes J
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1 STCCGYRMCVPC 12
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 525
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LENGTH: 12
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Gaps

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Score 63; DB 14; Length 13; Pred. No. 0.045; 2; Mismatches 2; Indels

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Pred. No. 0.045;
2; Mismatches 1; Indels
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APPLICANT: Schoenfeld, Robert M.
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Shatty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
WUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 535
                                                                                                                          ; Sequence 535, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
                                                                                                                                                                                                 Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
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72.7%;
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                     1 STCCGFKMCIPC 12
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Pred. No. 0.045;
2; Mismatches 2; Indels
                                                                                     APPLICANT: University of Utah Research Foundation
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CURRENT APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SENGTHALE.
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CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
FRICR APPLICATION NUMBER: US 60/267,408
FRICR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 13
                                                                                                                                                                                                 APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Malker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 355, Application US/10072602B Publication No. US20030109670A1 GENERAL INFORMATION:
                    Sequence 538, Application US/10072602B Publication No. US20030109670A1 GENERAL INFORMATION:
                                                                                                              Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J, Michael
Watkins, Maren
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STCCGFKMCIPC 12
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ORGANISM: Conus textile
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US-10-072-602B-538
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Pred. No. 0.17;
0; Mismatches 1; Indels
                                                                          79.7%; Score 63; DB 14; Length 16; 72.7%; Pred. No. 0.053; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-072-602B-62
is Sequence 62, Application US/10072602B
j Publication No. US20030109670A1
j GENERAL INFORMATION:
j APPLICANT: University of Utah Research Foundation
j APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
j APPLICANT: McIntosh, J, Michael
j APPLICANT: Watkins, Maren
j APPLICANT: Watkins, Maren
j APPLICANT: Garrett, James B.
The APPLICANT: Colivera B.
The A
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CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patentin version 3.0
SEQ ID NO 62
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Grilley, Michelle
Schoenfeld, Robert M.
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity
Matches 8; Conserv
US-10-072-602B-355
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 10, 2004, 16:00:00; Search time 3.72973 Seconds (without alignments) 309.486 Million cell updates/sec Run on:

US-10-072-602B-534 79 1 SVCCGYKLCFPC 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result		Query				
No.	Score	Match	Length	DB	ID	cription
-	53	67.1	258	. 2	T30368	probable immediate
7	20	63.3	55	7	S25774	testis-specific pr
6	20	63.3	514	7	T10559	hypothetical prote
4	49	62.0	428	7	T46025	
5	47	59.5	245	7	040	
9	47	59.5	373	7	T47488	pro
7	47	59.5	470	7	C86256	
80	47	59.5	525	7	T10574	
σ	44	55.7	342	П	F64141	യ
10	44	55.7	361	N	T12543	hypothetical prote
11	43	54.4	78	ď	T50943	н
12	43	54.4	186	7	A45910	ultra-high-sulfur
13	43	54.4	222	7	T47487	hypothetical prote
14	43	54.4	373	7	E84647	
15	43	54.4	484	7	T20254	_
16	43	54.4	629	ď	T01520	_
	42	53.2	350	~1	G84647	cal
	42	53.2	434	~	A43252	probable transcrip
	42	53.2	512	~	F86193	hypothetical prote
20	42	3	628	7	F85024	
21	42		715	7	S77439	hypothetical prote
22	41		69	~	A96696	protein FIN21.2 [i
23	41	51.9	137	7	G96779	probable RING zinc
24	41		193	~	T09043	hypothetical prote
25	41		226	~		1801
26	41	٠.	227	7	241	probable RING zinc
27	41	51.9	235	7	$\sim$	cal
28	41		4	7	T52142	finger p
29	41	51.9	9	7	m	٠,

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Gaps

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Query Match 63.3%; Score 50; DB 2; Length 55; Best Local Similarity 70.0%; Pred. No. 1.5; Matches 7; Conservative 0; Mismatches 3; Indels

homeodomain transc	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical 216.5	protein C27A12.8 [	protein C27A12.7 [	hypothetical prote	granulocyte colony	similar to Ariadne	lymphocyte antigen	ZK652.5 protein -	hypothetical prote	erythrocyte membra	chloride channel p
H84443	T52522	T02396	T21000	JQ2183	H87793	G87793	T09063	A24573	A84725	S29498	S44908	T47727	T18396	T07608
90	4 7	7	7	~	N	N	7	N	7	7	7	7	7	7
332	402	404	890	1885	436	497	180	207	542	267	580	719	1729	764
51.9	51.9	51.9	51.9	51.9	51.3	51.3	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.0
41	41	41	41	41	40.5	40.5	40	40	40	40	40	40	40	39.5
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

	RESULT 1
	T30368
	probable immediate early transactivator 0 - Lymantria dispar nuclear polyhedrosis virus
	Cispecies: Lymantria dispar inclear polyhedrosis virus, Ldwnby
	Cidace: 29-Oct-1999 #Bequence_leviblon 59-Oct-1999 #teAt_Chainge 29-Oct-1999 CiArcession: T30368
	R.Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
-	Virology 253, 17-34, 1999
	A, Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
	A) Reference number: Z20836; MUID:99124785; PMID:9887315
	A A A COG SESION: 130 SES
	A ASCALUS: PIETIMITIALY; CIGHISTACEU IION GB/EMBL/UDBU
	A:Residues: 1-558 <kktz></kktz>
-	A; Cross-references: EMBL: AF081810; PIDN: AAC70206.1
	C;Keywords: immediate-early protein
· · · ·	Query Match 67.1%; Score 53; DB 2; Length 258;
	ative 3
	Qy 1 SVCCGYKLCFPC 12
	RESULT 2
	525/74 testis-specific protein Mst84Dc - fruit fly (Drosophila melanogaster)
	C;Species: Drosophila melanogaster
	C;Date: 26-Jul_1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
	CyAccession: S25/74; C56565
	K.Kuun, K.; Kunn, V.; Boerscn, D.; Glaeczer, K.H.; Schaefer, D.; Schaefer, M. Mech. Dev. 35, 143-151, 1991
	A:Title: A cluster of four genes selectively expressed in the male germ line of Drosophi
	A; Reference number: A56565; MUID:92102953; PMID:1684716
	A;Accession: S25774
	A; Molecule type: DNA
	A;Residues: 1-55 <kuh></kuh>
	A;Cross-references: BMBL:X67703; NID:g11072; PIDN:CAA47939.1; PID:g11075
	A; Note: the authors translated the codon IGC for residue 55 as Throng
	A;Note: orquence extracted from Num Dackbone (Numbr), Numbr:/4222)
·	A:Gene: Mst81DC
	A;Cross-references: FlyBase:FBgn0004174
	A,Map position: 3
	C, Superfamily: fruit fly testis-specific protein
	C;Keywords: spermatogenesis; tandem repeat

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Gaps

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hypothetical protein F9K21.60 - Arabidopsis thaliana (S.Speciesa Arabidopsis thaliana (mouse-ear cress) (S.Speciesa: Arabidopsis thaliana (mouse-ear cress) (C.Speciesa: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 (C.Accession: T47488 ** Analysis 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotherical protein [imported] - Arabidopsis thaliana (Socies: Arabidopsis thaliana (mouse-ear cress) (C.) Date: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (C.) Date: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (C.) Accession: C86256 (C.) Accession: C. W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 (C.) Accession: C., In, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Mul D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Mul D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Miller: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Accession: C86256 (A.) Ashacession: C86256 (A.) Ashacession: C86226
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A;Molecule type: DNA
A;Residues: 1-470 <STO>
A;Cross-references: GB:AE005172; NID:gl0086520; PIDN:AAG12580.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 2; Length 245; Pred. No. 11; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 373;
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                                                                                                  A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DMR
A,Residues: 1.245 cAHRA
A,Cross-references: EMBL:U75930; NID:g2934903; PID:g1911384
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A; Reference number: Z17011; MUID: 97271300; PMID: 9126251
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Pred. No. 18;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         59.5%;
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A, Cross-references: EMBL:AL138657
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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A;Introns: 92/3; 328/2; 353/3
A;Note: F9K21.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 CCOYSLCYAC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CCGYKLCFPC 12
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A; Status: preliminary
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                                                        A; Accession: T10407
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                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F25E4.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T10559
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro submitted to the Protein Sequence Database, June 1999
A;Accession: T10559
A;Accession: T10559
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-514 cBEV>
A;Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.10
A;Experimental source: cultivar Columbia; BAC clone F25E4
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Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T10K17.240 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T46025
R;Benes, V.; Wurmbach, B.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.;
Submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23019
A;Accession: T46025
A;Accession: T46025
A;Accession: T4602
A;Acc
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C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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63.3%; Score 50; DB 2;
Best Local Similarity 70.0%; Pred. No. 7.3;
Matches 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%; Score 49; DB 2;
60.0%; Pred. No. 8.8;
iive 2; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Map position: 4
A, Introns: 436/3; 457/3; 479/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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                                              CCGYKLCFPC 12
                                                                                                                                                CCGYYCCGPC 18
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A;Gene: ATSP:F25E4.10
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C;Superfamily: RING
F;127-176/homein:
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C;Accession: A45910
R;McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.
Livvest. Dermatol. 92, 263-266, 1989
A;Title: An ultra-high sulfur Keratin gene is expressed specifically during hair growth. A;Reference number: A45910; MUID:89140394; PMID:2465353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable ferredoxin DitA [imported] - Pseudomonas abietaniphila
C;Species: Pseudomonas abietaniphila
C;Species: Pseudomonas abietaniphila
C;Species: Pseudomonas abietaniphila
C;Accession: T50943
R;Martin, V.J.; Mohn, W.W.
B;Martin, V.J.; Mohn, W.W.
A;Ederence number: Z25281; MUID:99235742; PMID:10217753
A;Accession: T50943
A;Accession: T50943
A;Accession: T50943
A;Accession: T50943
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: DNA
A;Residues: 1-78 cMAR>
A;Resi
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Accession: T1254
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
B;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
A;Reference number: 217524
A;Reference number: 217524
A;Reference number: 217524
A;Status: preliminary
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-361 **MAM**
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C;Species: Mus musculus (house mouse)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
*Residues: 1-186 <MCN.
A;Cross-references: GB:M27685; NID:g341749; PIDN:AAA81560.1; PID:g1066818
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 18;
0; Mismatches 2; Indels
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C, Genetics:
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60.0%; Pred. No. 34;
tive 0; Mismatches
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39;
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Pred. No.
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75.0%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F25E4.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T10574
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancrd submitted to the Protein Sequence Database, June 1999
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A;Molecule specific acid sequence not shown; translation not shown
A;Molecule 1-342 <TIGR>
A;Cross-references: GB:U32690; GB:L42023; NID:g1572991; PIDN:AAC21731.1; PID:g1573000;
C;Function:
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A,Molecule type: DNA
A,Residues: 1-525 <BEV>
A,Residues: 1-525 <BEV
A,Cross-references: EMBL.AL050399; GSPDB:GN00062; ATSP:F25E4.160
A,Experimental source: cultivar Columbia; BAC clone F25E4
C,Genetics:
A,Gene: ATSP:F25E4.160
A,Map position: 4
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Pred. No. 19;
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T12543
hypothetical protein DKFZp434M154.1 - human (fragment)
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Best Local Similarity 63.0.
The 7; Conservative
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VCCGQ--CYPC 100
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                                                                                                                                                  283 CTGYKYCFP 291
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                                                                    CCGYKLCFP 11
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Length 484; 2; Indels

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A Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Cross-references: 1-484
A; Experimental source: clone C55A6
C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: C55A6.1
A; Map position: 5
A; Introns: 84/1; 102/1; 220/3; 275/1; 298/3; 331/2; 464/3
C; Superfamily: RING finger homology
F; 8-57/Domain: RING finger homology <RN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.4%; Score 43; DB 66.7%; Pred. No. 66; tive 1; Mismatches
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Best Local Similarity 66.7;
Matches 6; Conservative
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28 CGHKFCFIC 36
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47487
C;Accession: T47487
Submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
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A;Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Status: preliminary
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R;Kershaw, J.
A;Reference number: Z19243
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Bulaj G., Vyazovkina A., Yoshikami D., Cruz L.J., Olivera B.M.;
"Isolation and characterization of a novel conus peptide with apparent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 49-61, SYNTHESIS, MASS SPECTROMETRY, AND STRUCTURE BY NMR
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                                                                                                                                                      "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the
                                                                                                                                     "Two new classes of conopeptides inhibit the alphal-adrenoceptor and
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MEDLINE=20564325; PubMed=10988292;
Balaji R.A., Obtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H.;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoctation update)
Lambda-conotoxin CMrVIB precursor (Chi-conotoxin MrIA) (Chi-MrIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Venom;
MEDLINE=21419681; PubMed=11528421;
Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
                                                                               Thomas L., Adams D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus marmoreus (Marble cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Aeogastropoda; Conoidea; Conidae; Conus.
                                                                        Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D
Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
Lewis R.J.;
                                                                                                                                                                                                                                                                                 11-Hyp-12.
--- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
---- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
PDB; 1IEO; 03-APR-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SEQUENCE OF 49-61, SYNTHESIS, AND MASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 1; Length 13;
Pred. No. 0.00015;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROXYLATION.
277AAC376EAD2B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                              Neurotoxin; Toxin; Hydroxylation; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AA.
                  SYNTHESIS, AND STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 49-61, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antinociceptive activity.";
J. Biol. Chem. 275:32391-32397(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             venom of Conus marmoreus.";
J. Biol. Chem. 275:39516-39522(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                          MEDLINE=21419681; PubMed=11528421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20490660; PubMed=10900201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 86.1%;
Local Similarity 90.9%;
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Venom, and Venom duct
                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AA; 1382 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VCCGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   з уссеткиснее 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=42752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CXL2 CONMR
P58808:
                    SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                    MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (mr10a).
                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CXL2 CONMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Two new classes of conopeptides inhibit the alphal-adrenoceptor and noradrenaline transporter.";
Nat. Neurosci. 4:902-907(2001).
-!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
-!- SUBCEDIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                   -!- PTM: Exists in two forms, due to cis-trans isomerization at His-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
Seow K.I., Bay B.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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0
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Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoldea; Conidae; Conus.
                                                                                                                                                                           -!- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.
-!- SIMITARITY: Belongs to the chi/lambda-conotoxin family.
InterPro; IPR004214; Conotoxin.
Pfam: PF02250; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 1; Length or, Pred. No. 0.0006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 1; Length 12;
Pred. No. 0.016;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                LAMBDA-CONOTOXIN CMRVIB.
                                                                                                                                                                                                                                                                                                                                                                                             HYDROXYLATION.
F4DESB5A97EB8DBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277AAE2422D5A2C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lambda-conotoxin CMrX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROXYLATION.
                                                                                                                                                                                                                                                                 Neurotoxin; Toxin; Hydroxylation; Signal.
                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Venom;
MEDLINE=20564325; PubMed=10988292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 AA; 1251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                      6499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VCCGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 VCCGYKLCHPC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VCCGYKLCFPC 12
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EMBL outstation

and the

the Swiss Institute of Bioinformatics

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Wed Aug 11 13:19:38 2004
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Response, From N. A.

Response, F. C. Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Response, F.A., Lewis, S.E., Holt R.A., Sabburner M., Handerson S.N.,

Response, R.A., Lewis, S.E., Richards S., Ashburner M., Handerson S.N.,

Response, R.C., Rogers Y.-H.C., Blazel R.G., Chenn L.X.,

Response, R.C., Borgers Y.-H.C., Blazel R.G., Chenn L.X.,

Response, R.C., Barrer E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Response, M. M., Bestu A., Barkendale J., Bardari D., Botshakov S.,

Response, M.Y., Benos P.V., Berman B.P., Bardari D., Botshakov S.,

Response, M., Camber B. C., Barkendale J., Bardari D., Botshakov S.,

Response, M., Camber S., Danger S., Danger, B., Center A., Chandre P.

Response, M., Camber S., Danger S., Mays A.D., Dew I., Dietz S.M.,

Repholos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Repholos B., Delcher A., Bornes M. S., Botshakov S.,

Repholos B., Delcher A., Honger C., Ferraca S., Eleischmann W.,

Roslor C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,

Rolor C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,

Repton M. M., Maryer D.M., Hourby D., Morker D., Lin, X.,

Response, M., Marker S., Hourk P., Karaff C., Kravitz S., Kilp D., Lai Z.,

Lasko P., Lei Y. Levitsky A.A., Li J.H., Li L., Langer M., M.,

Reson K.M., Mow, M., Murphy B., Murphy L., Morshen D.,

Ra Merkulov G., Milshina N.V., Modarry C., Morris J., Mang Y., Lin X.,

Reinert B.C., Siden K.A., Nowley, M., Stupsker M., Smith T.,

Ra Reinert K., Remington K., Saunders R., Pollard J., Puri, Van S.,

Ra Shirekas R., Tector C., Turrer R., Venter E., Shen H.,

Ra Spier E., Spradling A.C., Scapleton M., Stupsker M., San S.,

Ra Shirekas R., Tector C., Turrer R., Venter E., Shen H.,

Ranger R., Shanger P., Reinert R., Wenter E., Shen H.,

Ranger R., Shong F.N., Robing W., Venter B., San X., Smith H.O.,

Ranger R., Melson P., Reinert R., Scholes R., Smith R.,

Ranger R., Shong F.N., Relance R., S
                                                                                                                                                                                                                                                                                                                                                                                                                     "A cluster of four genes selectively expressed in the male germ line of Drosophila melanogaster.";
Mech. Dev. 35:143-151(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Testis.
-!- DEVELOPMENTAL STAGE: Primary spermatocytes.
-!- DOMAIN: This protein is mostly composed of repetitive C-G-P
                                                                                                                                            Male specific more in management in Male specific more protein Mst84Dc.
MST84DC OR CG17945.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                              Kuhn R., Kuhn C., Boersch D., Gläetzer K.H., Schaefer U., Schaefer M.;
                                                            001644, Q9VIAO,
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                 55 AA.
                                                                                                                                                                                                                                                                                                                                   STRAIN=Oregon-R;
MEDLINE=92102953; Pubmed=1684716;
                                             STANDARD;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                             M84C DROME
  LT 5
DROME
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motifs.
-!- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.

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0
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 1; Length 245; Pred. No. 2.7; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                Length 55;
                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357F43B15F7B1029 CRC64;
                                                                                                                                                                                                           Spermatogenesis; Repeat, Multigene family.
SEQUENCE 55 AA; 5225 MW; 95A12F3AEC88BD6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                              Score 50; DB 1;
Pred. No. 0.25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007954; Baculo_IE-1.
InterPro; IPR001841; Znf_ring.
Pfam; PF05290; Baculo_IE-1; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RING-TYPE
                                                                                                                            EMBL, AE003672; AAF54025.1, -. PIR, S25774; S25774. PS25774. PS25774. PS19889; Flyase; Fegno004174; Mst84Dc. InterPro; IPR005634; MsSP. PF03940; MSSP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27117 MW;
                                                                                                               EMBL; X67703; CAA47939.1; -.
                                                                                                                                                                                                                                                              63.3%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [mmediate-early protein IE-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Early protein; Zinc-finger.
ZN_FING 195 240
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U75930; AAC59137.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 ČĆQÝSĽČYAĆ 222
                                                                                                                                                                                                                                                                                                                           3 CCGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                            CCGYYCCGPC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CCGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
IEO NPVOP
ID IEO NPVOP
AC 010369;
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503 AA

PRT;

STANDARD;

DROME

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                     Relischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soctt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Meidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC 1 (CATALYTIC) (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMILARITY).
100B07F9194E6594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC 1 (CATALYTIC) (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMILARITY).
                                                  01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
Hypothetical zinc-type alcohol dehydrogenase-like protein HI0053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.
                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00107; ADH zinc N; 1.
PROSITE; PS00059; ADH ZINC; FALSE NEG.
Hypothetical protein; Oxidoreductase; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                  342 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 10;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002328; ADH zinc.
InterPro; IPR002085; Adh zn family.
InterPro; IPR000205; NAD_BS.
                    PRT;
                                                                                                                                                                                                                          SECULENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 AA; 37429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32690; AAC21731.1; -. PIR; F64141; F64141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 63.6
                    STANDARD;
                                                                                                                                           Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P07846; 1SDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; HI0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family
                    Y053 HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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METAL
                                                                                                                              HI0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
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HAEIN
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92 VCCGQ--CYPC 100

RESULT

VCCGYKLCFPC 12

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Matches

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RC STRAIN=Berkeley:

RX MININE=20196006; PubMed=10731132;

RX Adama N.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adama N.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Adamatides F.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner W., Henderson S.N., RA Guton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Briton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Hardon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G., Ralluw R.M. Basu A., Baxendal J., Bayraktarolan C.R., Miklos G.L.G., Ralluw R.M., Basu A., Baxendal J., Bayraktarolan C.R., Miklos G.L.G., RA Berson K.Y., Banos P.V., Berman B.D., Bhandari D., Bolahakov S., Borkova D., Borcham M.R., Bouck J., Brokstein P., Britale R.M., Candey S., Dallke C., Davenport L.B., Davies P., Antris M., Candey S., Dallke C., Davenport L.B., Davies P., Antris M., Larsser K., Olowes M., Dugan Rocha S., Ra Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan Rocha S., Ra Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan Rocha S., Ra Gelbart W.M., Classer K., Glodek A., Gong F., Gorrell J.H., Gu Z., Ramison P., Harris M., Walush F., Karpen G.H., Ket E., Karpen G.H., Karten G.M., Rawitz S., Kulp D., Lai Z., Lasko P., Karpen G.H., Ket G., Ramison J.A., Retchum K.A., Kalush F., Karpen G.H., Karpen G.H., Raylor D.L., Nelson D.E., Nosher S., Pallazzolo M., Pittman G.S., Pal Murphy L., Rayloson M., Skupski M.P., Palazzolo M., Pittman G.S., Pal Sunders R.D. C., Scheeler F., Shen H., Shue B.C., Siden-Kianos I., Rayloson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Turner R. A. Stapson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Turner R. A. Ratibeton M., Skupsenbach J., Williams S.M., Wordage T., Raylon W., Zhang S., Yao Q.A., Ye J., Ye R., Marserman D.A., Raylon W., Zhang S., Zhu X., Smith H.O., Gibbs R.A., Myers B.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Mainly cytoplasmic.
-i- TISSUB SPECTIFICITY: Widely expressed, with prominent levels in the nervous system and female gonads.
-i- DEVELOPMENTAL STAGE: Expressed in all tissues throughout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Might act as an E3 ubiquitin-protein ligase, or as part of E3 complex, which accepts ubiquitin from specific E2 ubiquitin-conjugating enzymes, such as UBCD10/UBE2L3, and then transfers it
                                                                                                                                                                                                                                                                                                                                                    Aguilera M., Oliveros M., Martinez-Padron M., Barbas J.A., Ferrus Pariadne-1: a vital Drosophila gene is required in development and defines a new conserved family of ring-finger proteins."; Genetics 155:1231-1244(2000).
                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Interacts with UBCD10. Can form dimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibk
Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ariadne-1 protein (Ari-1).
ARI-1 OR ARI OR CG5659.
                                                                                                                                                                                                                                                                                                                                          MEDLINE=20341325; PubMed=10880484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       STRAIN=Oregon-R;
ARI1 DRC
Q94981;
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Dykert J., Rivier J.E., Gray W.R., Imperial J.S., DelaCruz R.G.,
Bycorning A., Terlau H., West P.J., Yoshikami D., Olivera B.M.;
"An O-glycosylated neuroexcitatory conus peptide.";
Biochemistry 37:16019-16025(1998).

-- FUNCTION: Rappa-A-conotoxins bind and inhibit voltage-sensitive
potassium channels. When injected intraperitoneally in fish, the
peptide induces a period of rapid swimming followed by a spastic
paralysis with silf fibrillating fins. At high doses, the peptide
development, with maximum levels reached during metamorphosis and maintained in the adult.
SIMILARITY: Contains 2 RING-type zinc fingers.
SIMILARITY: Contains 1 IBR-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C->Y: IN ARII-3; LETHAL PHENOTYPE AND NO LOSS OF INTERACTION WITH UBCDIO.

OAECCE256CFSECO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH UBCDIO.
COILED COIL (POTENTIAL).
C->Y: IN ARI1-2; LETHAL PHENOTYPE AND
LOSS OF INTERACTION WITH UBCDIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; From Property IBR; 2.
SMART; SM00847; IBR; 2.
SMART; SM00184; RING; 2.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Ubl conjugation pathway; Zinc-finger; Repeat; Coiled coil.
27 ASP-RICH (ACIDIC).
RSD-RICH (ACIDIC).
RSD-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 1; Length 503;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Koppa-A-conotoxin SIVA (Spasiic peptide).
Conus striatus (Striated cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X98309; CAA66953.1; -.
EMBL; A80310; CAA66954.1; -.
EMBL; AB003507; AAF46807.1; -.
FlyBase; FB90001418; ari-1.
InterPro; IPR002867; Znf CGHC.
InterPro; IPR01841; Znf—ring.
Pfam; PF01485; IBR; 1.
SMART; SM00647; IBR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503 AA; 58932 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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203
2291
133
341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
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CXK4 CONST
CXK4 CONST
CXK4 CONST
CX 28-FEB-
DT 28-FEB-
DE KAPPA-NA-
DE KAPPA-NA-
COC APOGGST
COC APOGGS
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   SOURCE STATE THE TELEFORM SOURCE SOUR
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RX MEDLINE=9713263; PubMed=9169867;
RA MEDLINE=9713263; PubMed=9169867;
RA Bargues M., Baron L., Becker A., Biteau N., Bloecker H., Blugeon C., Bardques M., Baron L., Becker A., Biteau N., Bloecker H., Blugeon C., Bardques M., Baront L., Becker F., Boskovic J., Careter F., Boskovic J., Carender F., Boskovic J., Carender F., Bolaveau T., del Rey F., Dujon B., Eide L.G., Hanemann V., Hankeln T., RA Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T., Raener C., Roester H., Lamanen P., Legros Y., Louis B.J., Moeller-Rieker S., Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N., Parea J., Perea J., E., Sarzen A.-M., Schaefer M., Salom D., Saluz H.P., Saiz J.E., Sarzen A.-M., Schaefer M., Schmidt B.R., Schneider C., Scholler P., Schwarz S., Vorstassell P., Verhassell P., Vissers S., Voet M., Volckaert G., Manbutt R., Wedler E., Wedler H., Woelfl S., Harris D.E., Hamiln N., Hunt S., Jones L., McConnor R., Dedman K., Gentles S., Hamiln N., Hunt S., Jones L., McConnor R., Dedman K., Gentles S., Hanlin N., Hunt S., Jones L., McConnor R., Dedman K., Gentles S., Walsh S.V., Barrell B.G., Dietrich F.S., Mulligan J.T., Allen E., RA Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Rohung E., Duncan M., Hunicke-Smith S., Hyman R.W., Komp C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptional adapter 2.
ADA2 OR YDR440W OR D9461.33.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceties;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=92346713; PubMed=1638630;
MEDLINE=92346713; PubMed=1638630;
MEDLINE=92346713; PubMed=1638630;
Mercus G.L., Prina B., Silverman N., Marcus G.A., Agapite J.,
Regier J.L., Triezenberg S.J., Quarente L.;
"Genetic isolation of ADA2: a potential transcriptional adaptor required for function of certain acidic activation domains.";
-!- SUBCELLUIAR LOCATION: SECTEUR.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- PIM: O-linked glycan consists of Hex3-HexNAc2 disaccharide (Probable).
(Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 30;
                                                                                                                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID. O-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                            -!- MASS SPECTROMETRY: MW=4084.2; METHOD=LSIMS.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily.
Toxin, Neurotoxin; Ionic channel inhibitor;
Potassium channel inhibitor; Hydroxylation; Amidation;
Pyrrolidone carboxylation arboxylation arboxylation arboxylation.
12 24 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                     758A8CC1F146D7D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42.5; DI
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 AA.
                                                                                                                                                                                                                                                                                                                                         HYDROXYLATION.
                                                                                                                                                                                                                                                                                                  HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                     HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                 AMIDATION
                                                                                                                                                                                                                                       PROBABLE
                                                                                                                                                                                                                 PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                           46.78;
                                                                                                                                                                                                                                                                                                                                                                                3166 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVCCGY---KLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                              53.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 TTCCGYDPGTMCPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                          17
17
22
23
30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA2 YEAST
                                                                                                                                                                                                          DISULFID
DISULFID
MOD RES
                                                                                                                                                                                                                                                                          CARBOHYD
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MOD RES
MOD RES
MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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As bachwari D. 10c H. 110 N. Wesedis D. Rakhama R. Schredet M.,

P. Schogen T. Shreff N. William A. Yellow M., Doctetin D. D.

B. Davis R. W. Johnston M., Andrews S., Brinkama R., Cooper J., Ding H.,

B. Davis R. W. Johnston M., Andrews S., Brinkama R., Cooper J., Ding H.,

B. Mitsten J. Knoch T., Landon D., Catture B. S., Georg. T., Hallwarth K.,

B. Hawkins J. Hillist L.W. Jife M., Johnston D., Ochston M.,

B. Mitsten J. Knoch T., Langason W., Andrews S., Brinkama R., Cooper J., Hallwarth R.,

B. Mannas S., William N., Manna M., Fullewill P., Cohnston M.,

R. Madin W., Millon N., Manna M., Fullewill P., William S., Mannason W., Handlidgan P.,

Kithie K., Meses H. W., Zollner A., Zaccharomyces cerevisiae chromosome IV.;

R. Mature 391-578 (1994).

R. Mannas Septiment W. Barger S., Milbranam K., Hani J., Heumann K.,

R. Mannas Septiment W. Barger S., Milbranam K., Hani J., Heumann K.,

R. Mannas Septiment W. Barger S., Milbranam K., Hani J., Heumann K.,

R. Mannas Septiment W. Barger S., Milbranam K., Hani J., Heumann K.,

R. Mannas Septiment W. Barger S., Milbranam K., Manni J., Heumann K.,

R. Mannas Septiment W. Barger S., Milbranam K.,

R. Mannas Septiment W. Barger S.,

R. Mannas Septiment S.,

R. Mannas Septiment S.,

R. Mannas S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RN37 MOUSE STANDARD; PRT; 539 AA.
0925F4;
28-FBB-2003 (Rel. 41, Last sequence update)
28-FRB-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ring finger protein 37 (Ubiquitin conjugating enzyme 7 interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                    ;
0
                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical RING finger protein C16C10.7 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%; Score 41; DB 1; Length 235; 55.6%; Pred. No. 20;
                                                                     Score 42; DB 1; Length 434;
Pred. No. 25;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lloyd C.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 172 POLY-ALA.
235 AA; 24915 MW; 21A04AE951F6382A CRC64;
                                        50569 MW; 9637E1EDBBED0AC3 CRC64;
                                                                                                                                                                                                                                          235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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POLY-GLY.
POLY-ALA.
ZZ-TYPE
                                                                                                                                                                                                                                          PRT;
                            SWIRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00518, ZF RING 1, 1. PROSITE, PS50089, ZF RING 2, 1. Hypothetical protein, Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z46787; CAA86745.1; -. PIR; T19328; T19328. WormPep; C16610.7; CE01498. InterPro; IPR001841; Znf_ring. Pfam; PF00097; zf-C3HC4; 1. SMART; SMO184; RING; 1.
                                                                          53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.0.
Best Local Similarity
Conservative
                                                                                                       6; Conservative
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                     1 SVCCGYKLCFPC 12
                                                                                                                                                       ::| | | || || 23 AICPEYDLCVPC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 CGHLFCWPC 49
                                             434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                         Best Local Similarity
                                                                                                                                                                                                                                               CAEEL
 ZN FING
DNA BIND
DOMAIN
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                                             SEQUENCE
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                      C16C10.7
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RN37_MOUSE
ID RN37_MC
AC 0925F4,
DT 28-FEB-
DT 15-MAR,
DE Ring fi
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094941;
          RESULT 13
RN37 HUMAN
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               Pringa B., Martinez-Noel G., Muller U., Harbers K.,
"Interaction of the RING finger related U-box motif of a nuclear dot
protein with ubiquitin-conjugating enzymes.";
J. Biol. Chem. 276:19617-19623(2001).
                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.9%; Score 41; DB 1; Length 539; 66.7%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            539 AA; 58731 MW; 93F7372A9F888B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y -> C (IN REF. 2),
protein 5) (UbcM4-interacting protein 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                               conjugation pathway, Zinc-finger.
AIN 263 331 UBOX.
                                                          MEDLINE=21276466; PubMed=11274149;
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003613; Znf modRING.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00518; ZF_RING 1; 1. PROSITE; PS50089; ZF_RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF360997; AAK51467.1; -.
EMBL; BC025068; AAH25068.1; -.
       OR UBCE71P5 OR UIP5
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF04564; U-box; 1
SMART; SM00184; RING; 1
SMART; SM00504; Ubox; 1
                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:2154658; Rnf37
               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                  SEQUENCE FROM N.A.
                                                                                                      SEQUENCE FROM N.A.
                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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REPORTINE FROM N.A.

RADIUNE=21638749; PubMed=11780052;

RA MEDLINE=21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Deloukas P., Bates K.N., Beard L.M., Beare D.M.,

RA Bailey J., Barrilla R.E., Bates K.N., Beard L.M., Brown A.J.,

RA Beasley O.P., Blard C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.B., Dhami P.D., Dunn M.,

Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

Hamond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,

RA Ay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RAMINE S.A., Mistry D., Mocomachie L.J., McLay K., McMurray A.A.,

RA Mine S.A., Mistry D., Moore M.J.F., Mullikhn J.C., Nickerson T.,

RA Philliance B.J.C., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Tracey A., Tromans A.C., Vaudin M., Walliam S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

RA Wanner W. Roser M. T. Boott C.E., Sebra H.M., Bentley D.R., Beck S.,

RA Whitehead S.L., Whiteker P., Willey D.L., Williams S.A.,

RA Wanner W. Roser M. T., Boott C.E., Sebra M. Hilliams S.A.,

RA Whitehead S.L., Whiteker P., Willey D.L., Williams S.A.,

RA Whitehead S.L., Whiteker P., Willey D.L., Williams S.A.,

RA Wanner W. R. Wanner P. W., Hubbard T., Durbhin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Zeeberg B., Wagner L., Shamen C.F., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rourig A.C., Shevchenko Y., Bouffard G.G., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99156230, PubMed=10048485,
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
"Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                     28-FEB-2003 (Rel. 41, Created)
BeFEBS-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ring finger protein 37 (Ubiquitin conjugating enzyme 7 interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
     541 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for large proteins in vitro.";
DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                        RNF37 OR UBCE7IPS OR KIAA0860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 414:865-871(2001).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                    28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rogers J.;
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Gaps

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2; Indels

Pred. No. 42; 1; Mismatches

6; Conservative

||: || || CGHLLCRPC 510 4 CGYKLCFPC 12

ð g (See http://www.isb-sib.ch/announce/

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send an email to license@isb-sib.ch)
 requires a license agreement
                                                                                                                                                                                                                                                                                                                                       51.9%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colony-stimulating factor.";
EMBO J. 5:575-581(1986).
                                                 EMBL; D14996; BAA03641.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           CGYKLCF-----PC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Filgrastim) (Lenograstim)
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                            1885 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSF3_HUMAN
ID _CSF3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P09919:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
8-EE-2003 (Rel. 41, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (RNA replicase) (216.5 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apple chlorotic leaf spot virus.";
J. Gen. Virol. 74:1927-1931(1993).
-!- FUNCTION: PROBABLY INVOLVED IN VIRAL RNA REPLICATION.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA} (N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein) (ORF1).
Apple chlorotic leaf spot virus (isolate apple) (ACLSV).
Viruses; SRNA positive-strand viruses, no DNA stage; Flexiviridae;
Trichovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato K., Yoshikawa N., Takahashi T., "Complete nucleotide sequence of the genome of an apple isolate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: TO THE PUTATIVE REPLICATION-ASSOCIATED PROTEINS OF
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Bluterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Ghereration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBUNIT: Interacts with UBEZL3 (By similarity).
-!- SUBCRILUMAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 1 RING-type zinc finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 541;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41;
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                                                                                                                                                                                                                                                                                                                          EMBL; BC000515; AAH00515.1; -. InterPro; IPR003613; Znf modRING. InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=93389448; PubMed=8376968;
                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00184; RING; 1.
SMART; SM00504; UDox; 1.
PROSITE; PS500519; ZF RING 1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                          EMBL; AB020667; BAA74883.1; -. EMBL; AL121891; CAC09909.1; -.
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MEDLINE=86118679; PubMed=3484805;

MEDLINE=86118679; PubMed=3484805;

Hirata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,

Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;

"Moleoular Loining and expression of cDNA for human granulocyte
colony-stimulating factor.";

Nature 319:415-418(1986).
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01-MAR-1989 (Rel. 10, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnocation update)
Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoietin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Expression of granulocyte colony-stimulating factor by human cell
R InterPro; IPR00133; 20G-PeII Oxy.
R InterPro; IPR001323; 20G-PeII Oxy.
R InterPro; IPR001789; RNA_dep_RNApol2.
R InterPro; IPR001799; RNA_pol_DS_PS.
R InterPro; IPR007095; RNA_pol_DS_PS.
R InterPro; IPR007094; RNA_pol_DS_PS.
R InterPro; IPR007094; RNA_pol_PS_VI.
R Pfam; PF05413; Peptidase_C34; 1.
R Pfam; PF05413; Peptidase_C34; 1.
R Pfam; PF0543; Viral_helicase1; 1.
R Pfam; PF0543; Viral_helicase1; 1.
R Pfam; PF05443; Viral_helicase1; Nucleotide-binding; R Helicase; ATP-binding; RNA_clirected RNA_polymerase; Nucleotide-binding; RNA_clirected RNA_clirected RNA_polymerase; Nucleotide-binding; RNA_clirected RNA_clirec
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L.,
Nickerson D.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 1885;
Pred. No. 1.3e+02;
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POLYMERASE ACTIVE SITE
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MEDLINE=86220137; PubMed=2423327;
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*A" REPLIATE CORRAPHY (2.2 ANGSTROMS).

**MEDLINE=92381718; PubMed=7685117;

#Hill C.P., Osslund T.D., Eisenberg D.;

#The structure of granulocyte-colony-stimulating factor and its

relationship to other growth factors.";

Proc. Natl. Acad. Sci. U.S.A. 90:5167-5117 (1993).

-!-FUNCTION: GRANULOCYTE/RACROPHAGE COLONY-STIMULATING FACTORS ARE

CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,

DIFFERENTIATION, AND FONCTION OF 2 RELATED WHITE CELL POPULATIONS

OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
                                                                                                                                                      CARBOHYDRATE-LINKAGE SITE.
MEDLINE=93293942, PubMed=7685769,
CLOGAGEON C.L., Hu. S., Boone T.C., Lu H.S.;
"Glycosidase digestion, electrophoresis and chromatographic analysis of recombinant human granulocyte colony-stimulating factor glycoforms J. Chromatogr. A 637:55-62(1993).
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94304859; PubMed=7518249; Zink T., Ross A., Luers K., Cieslar C., Rudolph R., Holak T.A.; "Srructure and dynamics of the human granulocyte colony-stimulating factor determined by NMR spectroscopy. Loop mobility in a four-helix-
                         MEDLINE=86151684; PubMed=2420009;
Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,
Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
Barendt J., Platzer E., Moore M.A.S., Mertelsmann R., Welte K.;
"Recombinant human granulocyte colony-stimulating factor: effects on
normal and leukemic myeloid cells.";
Science 232:61-66(1986).
                                                                                                                                                                                                                                                                          STRUCTURE BY NMR.
MEDLINE=91106200; PubMed=1281794;
Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
Secondary structure of human granulocyte colony-stimulating factor derived from NMR spectroscopy.";
FESS Lett. 314:435-439(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 33:8453-8463(1994).
                SEQUENCE OF 19-207 FROM N.A.
                                                                                                                                                     CARBOHYDRATE-LINKAGE
                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bundle protein."
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Event=Alternative splicing; Named isoforms=2; IsoId=P09919-1; Sequence=Displayed; SUBUNIT: Monomer. SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS:

ISOIG=P09919-2; Sequence=VSP 002673; PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH CAN BE MODIFIED WITH UP TO TWO SIALIC ACID RESIDUES (DONE IN RECOMBINANTLY EXPRESSED G-CSF FROM CHO CELLS). Name=Short;

PHARMACEUTICAL: Available under the names Neupogen or Granulokine (Amgen/Roche) and Granocyte (Rhone-Poulenc). Used to treat neutropenia (a disorder characterized by an extremely low number of neutrophils in blood).

SIMILARITY: Belongs to the IL-6 superfamily.

CAUTION: REF.4 MISQUOTES THE GENE NAME AS "CSFI".

DATABASE: NAME=Neupogen/Granulokine;

NUTE-CLINICAL information on Neupogen/Granulokine;

WWW="http://www.neupogen.com/"

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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                                                                                                                                       GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005130; F:granulocyte colony-stimulating factor recep. . .; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
InterPro; IPR003529; GCSF MGF.
InterPro; IPR003573; IL6_MGF_GCSF.
Pfam; PF00489; IL6; IL
                                                                                                                                                                                                          PRINTS; PRO0433; ILGGSSFMGF.
Probom; PD008388; GCSF_MGF; 1.
SMART; SM00126; IL6; 1.
PROSTIE; PS00254; INTERLEUKIN_6; 1.
Cytokine; Growth factor; Glycoprotein; Signal; Alternative splicing; Polymorphism; Pharmaceutical; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                 GRANULOCYTE COLONY-STIMULATING FACTOR
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Missing (in isoform/FTId=VSP_002673.
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    , X03438; CAA27168.1; -. ; M13008; AAA03056.1; -. ; X03665; CAA27291.1; -. ; X03655; CAA27290.1; -. ; AF380025; AAK62469.1; -. ;
                                                M17706; AAA35882.1; -. A24573; A24573.
X03438; CAA27168.1;
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1RHG; 31-JAN-94.

1GNC; 31-JUL-94.

1CD9; 08-MAR-00.

1PGR; 08-MAR-00.
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MIM; 138970; -.
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Search completed: August 10, 2004, 16:03:05 Job time : 3.59459 secs Sunk Sieut

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1: sp archea:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	Q9bpe9 conus penna	09ibq9 spodoptera	Q801s1 adoxophyes	036453 lymantria d	Q96bq3 homo sapien	Ol0614 helicoverpa	Q8v5x4 helicoverpa	Q99h38 helicoverpa	091d86 arabidopsis	Q9m2p5 arabidopsis	Q8rxf2 arabidopsis	Q7xif9 oryza sativ	Q9m1f9 arabidopsis	Q9fww3 arabidopsis	09le85 arabidopsis	Q9hjh7 thermoplasm
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RESULT 2 Q9IBQ9

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Q9R6Z5 Q8SU59 Q8QL66 Q8U1Y7 Q95V29 Q97Z6 Q9UU35 Q9UU35 Q9U122 Q9D122 Q9D122 Q9BL8 Q9D122 Q8BL9 Q9BL8 Q	ALIGNMENTS	PRT;	Created) Last seq Last ann	one). 1; Gastropoda oda; Sorbeocol iidae; Conus.	.58371; .vidan N.	ervariab 	Score 63; Pred. No. 2; Mismat	
2			17, 17, 25,	ed cusca ropo con	=111	Hyp 131( .1; ellu acti enes otox	. 7 %;	
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		PRE	(F)	deta feta fa; fa; fa;	OM N 0596 3.G.	for for 3003 376; 376; 376; 376; 376; 370;	Con	70GY
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GO; GO:0006118; P:electron transport; IEA.
InterPro; IRR007954; Baculo IE-1.
InterPro; IRR001945; CytC_heme_BS.
InterPro; IRR001841; Znf_ring.
Pfam; PF05290; Baculo IE-1; 1.
PROSITE; PS00190; CYTCHROME_C; 1.
PROSITE; PS00199; ZF RING _2; 1.
SEQUENCE 243 AA; Z8756_MW; SD72075190E974A5 CRC64;
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InterPro; IPR007954; Baculo_IE-1.
InterPro; IPR001841; Znf_ring.
Pfam; PF02290; Baculo_IE-1; 1.
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58.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lymantria dispar.";
Virology 253:17-34(1999).
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nes 6, Conservative
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Best Local Similarity
7; Conserva
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                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                              Vlak J.M.;
"Baculoviruses contain a gene for the large subunit of ribonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ADNO01;
Nakai M., Goto C., Kang W., Shikata M., Kunimi Y.;
Nakai M., Goto C., Kang W., Shikata M., Kunimi Y.;
Sequence and genome organization of a nucleopolyhedrovirus isolated from the smaller tea tortrix, Adoxophyes honmai.";
Submitted (MAR-2023) to the EMBL/GenBank/DDBJ databases.
EMBL; ARD065270; BAC65276.1; -.
GO; GO:0005489; F:electron transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

IJKel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.;

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF169823; AAF33667.1; -.

InterPro; IPR007954; Baculo IE-1.

InterPro; IPR001941; Znf_ring.

Pfam; PF05290; Baculo IE-1; 1.

SMART; SM0184; RING; 1.

PROSITE; P850089; ZF RING 2; 1.

SEQUENCE 244 AA; Z8719 WW; IF7662E837A866DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                               MEDLINE=20036646; PubMed=10567663;
IJKel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
Goldbach R.W., Vlak J.M.;
"Sequence and organization of the spodoptera exigua multicapsid
nucleopolyhedrovirus genome.";
J. Gen. Virol. 80:3289-3304(1999).
                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A.
MEDLINE=97437494; PubMed=9292027;
van Strien E.A., Faktor O., Hu Z.H., Zuidema D., Goldbach R.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zuidema D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                      Spodoptera exigua nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID=224199;
                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q80LS1;
01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
     244 AA
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   PRT;
                                                                                                                                                                                                                                                                                              Gen. Virol, 78:2365-2377(1997).
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   PRELIMINARY;
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   Q9IBQ9;
Q9IBQ9;
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99124785; PubMed=9887315;
Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
Slavicek J.M., Rohrmann G.F.;
"Sequence and analysis of the genome of a baculovirus pathogenic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2003 (TrEMBLrel. 24, Last annotation update)
Immediate early 0 protein (Immediate early transactivator 0).
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Slavicek J., Rohrmann G.F.;
67.1%; Score 53; DB 12; Length 243; 60.0%; Pred. No. 0.6;
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Pred. No. 0.63;
3; Mismatches 2; Indels
                                                                   Indels
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50089; ZF RING 2; 1.
SEQUENCE 258 AA; Z9395 MW; AC564CDF92282BAD CRC64;
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                                                                   2; Mismatches
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Gaps

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Q96BQ3

RESULT 5

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Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F., Presnail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M., "Genome sequence analysis of Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AS34030, AALSA13.1;

InterPro; IPR001841; Znf ring.

InterPro; IPR001841; Znf ring.

SMART; SM00184; RBUNG: 1.

PROSITE; PS50089; ZF RING: 2;

SRQUENCE Z85 AA; 33189 MW; EF9E35A71B8E7F3D CRC64;
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Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
Sequence analysis of the gp37 gene of Heliothis armigera single-nucleocapsid nucleocopyhedrovirus.";
Zhongguo Bingduxue 15:35-42(2000).
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Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
"Sequence analysis of the iap3 gene of Heliothis armigera single-
                                                             63.3%; Score 50; DB 12; Length 151; 70.0%; Pred. No. 1.2; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.3%; Score 50; DB 12; Length 285; 70.0%; Pred. No. 2.1; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
PROSITE; PS50089; ZF RING 2; 1.
SEQUENCE 151 AA; 17548 MW; 4986432F6DCD3169 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae,
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Helicoverpa armigera nuclear polyhedrosis virus.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                      7; Conservative
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                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                    101 CCGYKICNLC 110
                                                                                                                                              3 CCGYKLCFPC 12
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NCBI_TaxID=10468;
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                                                                              Local Similarity
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                                                                Query Match
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Q99H38;
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Matches
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCSI_TaxID=9606;
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MEDLINE=97321796; PubMed=9178498;
Le T.H., Wu T., Robertson A., Bulach D., Cowan P., Goodge K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetically variable triplet repeats in a RING-finger ORF of Helicoverpa species baculoviruses.";
Virus Res. 49:67-77(1997).
                                                                                                                                                                                                                                                                                                                             A Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!-STMILARITY: CONTAINS I RING-TYPE ZINC FINGER.
R BHBL; BCO15353; AAR15353.1; -.
Genew; HGNC:19015; TRIM43.
R GJ; GO:0005622; C:intracellular; IEA.
GG; GO:000570; F:zinc ion binding; IEA.
R InterPro; IPR001870; B302.
R InterPro; IPR001870; SPRY receptor.
InterPro; IPR001815; Znf Bbox.
R InterPro; IPR001841; Znf Ebox.
R InterPro; IPR001841; Znf Ebox.
R Pfam; PF00622; SPRY; 1.
R Pfam; PF00623; Zf-B box; 1.
R Pfam; PR00623; Zf-B box; 1.
R Pfam; PR00623; Zf-B box; 1.
R Pfam; PR00623; Zf-GB box; 1.
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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PROSITE; PS50119; ZF BBOX; 1.

PROSITE; PS00518; ZF RING 1; 1.

PROSITE; PS50089; ZF RING 2; 1.

Hypothetical protein; Metal-binding; Zinc; Zinc-finger.

SEQUENCE 446 AA; 52265 MW; 805E4AA25617724A CRC64;
                                                                                                            Created)
Last sequence update)
Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUM-1997 (TrEMBLrel. 24, Last annotation update)
ACMNPV ORF1 homolog.
                                                                          446 AA
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InterPro; IPR007954; Baculo_IE-1.
InterPro; IPR001841; Znf ring.
Pfam; PF05290; Baculo_IE-1; 1.
SMART; SM00184; RING; 1.
                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 101-OCT-2003 (TrEMBLrel. 25, 14) Pypochetical protein. Homo sapiens (Human).
                                                                      PRELIMINARY;
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Matches 6; Conservative
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27 TICCGHSFCRPC 38
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
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SEQUENCE FROM N.A.
Benes V., Wurmbach E., Drzonek H., Ansorge W., Mewes H.W., Lemcke K.,
Banes V., Wurmbach E., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL161531; CAB82144.1; --
PIR; T10559; T10559.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005189; F:electron transport; IEA.
GO; GO:000718; F:electron transport; IEA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR00345; CytC heme BS.
InterPro; IPR004446; DGI.
InterPro; IPR004446; DGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 428 AA; 47856 MW; D5F832A2E7BC16C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59336 MW; E05CF4148B9D872F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.3%; Score 50; DB 10; 70.0%; Pred. No. 3.3; tive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.1;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03107; DC1; 2.
SMART; SM00109; C1; 3.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS01357; ZF_ZZ_1; 1.
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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SEOUENCE 514 AA; 5
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nes 7; Conserv
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                                                                                                                                                        SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
MEDLINE=21078302; PubMed=11210934;
Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
"Nucleotide sequence and transcriptional analysis of a putative basic
DNA-binding protein of Helioverpa armigera polyhedrovirus.";
Virus Genes 22:113-120(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
MEDLINE=21064569; PubMed=11125177;
Chen X., Jürle W.F., Tarchini R., Sun X., Sandbrink H., Wang H.
Peters S., Zuldema D., Lankhorst R.K., Vlak J.M., Hu Z.;
"The sequence of the Heliocoverpa armigera single-nucleocapsid nucleopolyhedrovirus genome.";
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SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4;
Chen X., 1JKel W.F., Tarchini R., Sun X., Sandbrink H., Wang
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.,
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 2.1;
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PROSITE; PS50089; ZF RING 2; 1.
SEQUENCE 285 AA; 33186 MM; CSFC3AE65BA27BDD CRC64;
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Arabidopsis thaliana (Mouse-ear cress).
                      nucleocapsid nucleopolyhedrovirus.";
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                                                            Zhongguo Bingduxue 15:43-49(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gen. Virol. 82:241-257(2001).
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70.0%;
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Jordan N., Bangert S., Wiedelmann R., Voss H., Unseld M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                   clone:P0005E02.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004259; BAC79716.1; -.
                                                                                                       2259 AA; 251175 MW; 70D2167D74B55EAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL138657; CAB75477.1; -.
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Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 373 AA; 42688 MW; A4484B5BF00667BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                Score 48; DB 10;
Pred. No. 23;
2; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                  373 AA
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                                                                                                                                                                                          2;
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InterPro, IPR002867; Znf_C6HC.
InterPro, IPR001841; Znf_ring.
                                                                                                                                              60.8%;
58.3%;
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                                                                                                                                                                                                                                                                         SLCCEYKINLPC 726
                                                                                                                                                                  Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00647; IBR; 1.
SMART; SM00184; RING; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01485; IBR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 CGYKFCYAC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                           715
                                                                                                       SEQUENCE
                                                                                     Helicase
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    Q9M1F9;
                                                                                                                                                                                                                                                                                                                                                                                Q9M1F9
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                                                                                                                                                                                                                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                                                                                                                                          D9M1F9
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  SOWRER
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Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,

A Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kaniya A.,

Rarlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,

Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,

RY Yarabidopsis ORF clones."

R Arabidopsis ORF clones."

L SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

BRBL; BY006585; AAP31929.1; -

C -: SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

BRBL; BY006585; AAP31929.1; -

DR InterPro; IPR001841; Znf ring.

BRBL; BY006585; AAP31929.1; -

BRBL; BY006585; AAP31929.1; -

BRBL; BY006585; AAP31929.1; -

BRBL; BY006585; AAP31929.1; -

BRRL; BY00689; ZF RING 1; 1.

BROSITE; PS50089; ZF RING 2; 1.

RWW PROSITE; PS50089; ZF RING 2; 1.

RWW HYPOCHELical protein; Metal-binding; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    °,
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                      Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.0%; Score 49; DB 10; Length 436; 60.0%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chromodomain helicase DNA binding protein-like protein.
                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Atag88030).
                                                                          436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 CCGHLYCWPC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CCGYKLCFPC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39947;
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                                                                                         Q8RXF2;
                                                                    Q8RXF2
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Gaps

0,

Indels

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Q7XIF9

RESULT 12

Q7XIF9

Best Loca Matches

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Length 373;

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PERCUENCE FROM N.A.

PRECEDED IN. Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
Lander E., Chao Q., Chin C., Khan S., Kim C., Koo T., Lee J.M.,
Lenz C., Liu A., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H.,
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
BRBL; AC022522; AGG12580.1; -.
RPIR; C86256, C86256.
GO, GO.000449; F: Emonoxygenase activity; IEA.
GO, GO.000449; F: Emonoxygenase activity; IEA.
RO; GO:000418; P: electron transport; IEA.
CO; GO:000418; P: electron transport; IEA.
RICEPPO; IPR000127; FAD pyr redox.
InterPro; IPR000205; NAD BY.
InterPro; IPR00043; FNAU_Cont_mnoxgn.
RICEPPO; IPR0043; FNAU_Cont_mnoxgn.
RICEPPO; PRO043; FNAU_Cont_mnoxgn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
Mewes H.W., Lemck K., Mayer K.F.X.;
Mewes H.W., Lemck K., Mayer K.F.X.;
Mewes H.W., Lemck K., Mayer R.F.X.;
Mewes H.W., Lemck K., Mayer R.F.X.;
Rembi. All61532; CAB62159.1; -.
Rembi. All61532; CAB63159.1; -.
Rembi. All61532; CAB63197.1; -.
Rempi. PR031317; DCI. All6158; CytC heme BS.
Refer: PR031317; DCI. 3.
Refer: PR03132; CAB63146; DCI. 3.
Refer: PR03132; CAB63146; DCI. 3.
Refer: PR03132; CAB63146; DCI. 4.
Refer: PR03132; CAB63146; DCI. 4.
Refer: PR03132; CAB63146; DCI. 4.
Refer: PR03132; CAB63144; DCI. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%; Score 47; DB 10; Length 470; 77.8%; Pred, No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60740 MW; 069557044AB56D4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53837 MW; 6345C99AE5110919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00419; ADXEDTASE.
PRINTS; PR00368; FADPNR.
PRINTS; PR00370; FMOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TEMBLES 15, 01-0CT-2000 (TEMBLES 15, 01-0CT-2003 (TEMBLES 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 CTGYKYCFP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
525 AA; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CCGYKLCFP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q9LE85
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Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 4 CGYKLCFPC 12

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Db 433 CGYVLCFDC 441

Search completed: August 10, 2004, 16:04:23

Job time: 11.8649 secs
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